

Devil, B.
09/1388090

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FILE 'HCAPLUS' ENTERED AT 12:28:27 ON 14 JUN 2002

L1 13560 SEA FILE=HCAPLUS ABB=ON PLU=ON ((NUCLEIC OR DNA OR
DEOXYRIBONUCLEIC OR DEOXY RIBONUCLEIC) (S) NUCLEOTIDE) (S) (P
OLYPEPTIDE OR POLYPROTEIN OR PROTEIN OR PEPTIDE)
L2 37 SEA FILE=HCAPLUS ABB=ON PLU=ON L1(S) (NEISSER? OR
(NEISSER? OR N) (W) (GONOCOCC? OR GONORRH? OR CATARRHAL?
OR LACTAMIC? OR OVIS OR LACUNATA OR BOVIS OR OSLOENSIS))
L5 21 SEA FILE=HCAPLUS ABB=ON PLU=ON L2 AND ENCOD?

L5 ANSWER 1 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2001:565074 HCAPLUS

DOCUMENT NUMBER: 135:151626

TITLE: Proteins comprising conserved regions of
Neisseria meningitidis surface antigen NhhA
Peak, Ian Richard Anselm; Jennings, Michael Paul
INVENTOR(S): University of Queensland, Australia
PATENT ASSIGNEE(S): PCT Int. Appl., 91 pp.
SOURCE: CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001055182	A1	20010802	WO 2001-AU69	20010125
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: US 2000-177917P P 20000125

AB Novel proteins that constitute modified forms of a Neisseria meningitidis surface antigen and **encoding** nucleic acids are provided. The modified surface proteins are characterized by having deletions of non-conserved amino acids, and thereby being capable of eliciting cross-protective immune responses against Neisseria meningitidis. The invention extends to the use of the modified surface antigens in diagnostics, in therapeutic and prophylactic vaccines and in the design and/or screening of medicaments. The modified surface antigens are particularly useful in vaccines which effectively immunize against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen.

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:633382 HCAPLUS

DOCUMENT NUMBER: 134:111106

TITLE: Nucleotide sequence of a three gene cluster in

Searcher : Shears 308-4994

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AUTHOR(S): Neisseria gonorrhoeae **encoding**
CORPORATE SOURCE: ribosomal proteins S6, S18, and L9
Ropp, Patricia A.; Nicholas, Robert A.
Department of Pharmacology, University of North
Carolina at Chapel Hill, Chapel Hill, NC,
27599-7365, USA
SOURCE: DNA Sequence (1998), 9(5-6), 341-345
CODEN: DNSEES; ISSN: 1042-5179
PUBLISHER: Harwood Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A cluster of three genes, rpsF, rpsR, and rplI, **encoding**
the ribosomal proteins S6, S18, and L9, resp., were cloned and
sequenced from Neisseria gonorrhoeae. The order of the genes within
the cluster was established as rpsF-rpsR-rplI. Within this cluster
an addnl. open reading frame of unknown identity spanning 108 bp was
found between rpsF and rpsR. The putative amino acid sequences
deduced from all three genes show a high degree of homol. to other
bacterial ribosomal proteins.

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR
THIS RECORD. ALL CITATIONS AVAILABLE IN
THE RE FORMAT

L5 ANSWER 3 OF 21 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:573939 HCAPLUS
DOCUMENT NUMBER: 133:160576
TITLE: Protein and DNA sequences of Neisseria gene
BASB064 and their uses in diagnosis and
vaccination
INVENTOR(S): Thonnard, Joelle
PATENT ASSIGNEE(S): Smithkline Beecham Biologicals S.A., Belg.
SOURCE: PCT Int. Appl., 79 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000047743	A1	20000817	WO 2000-EP888	20000204
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1151105	A1	20011107	EP 2000-903670	20000204
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
PRIORITY APPLN. INFO.:			GB 1999-2937	A 19990210
			WO 2000-EP888	W 20000204

AB The invention provides BASB064 polypeptides and polynucleotides **encoding** BASB064 polypeptides and methods for producing such polypeptides by recombinant techniques. Also provided are

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diagnostic, prophylactic and therapeutic uses. The invention provides protein and DNA sequences of *Neisseria meningitidis* gene BASB064, and methods for producing such polypeptides by recombinant techniques. Also provided are diagnostic, prophylactic and therapeutic uses.

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 4 OF 21 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:535269 HCAPLUS
DOCUMENT NUMBER: 133:130815
TITLE: Immunogenic protein BASB058 and its gene from *Neisseria meningitidis*
INVENTOR(S): Thonnard, Joelle
PATENT ASSIGNEE(S): Smithkline Beecham Biologicals S.A., Belg.
SOURCE: PCT Int. Appl., 79 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000044890	A1	20000803	WO 2000-EP560	20000125
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1153126	A1	20011114	EP 2000-903629	20000125
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			

PRIORITY APPLN. INFO.: GB 1999-2084 A 19990129
WO 2000-EP560 W 20000125

AB The invention provides BASB058 polypeptides and polynucleotides from *Neisseria meningitidis* serogroup B strain ATCC 13090 **encoding** BASB058 polypeptides and methods for producing such polypeptides by recombinant techniques. The BASB058 gene **encodes** a 107-amino acid protein with no similarities to known proteins. Also provided are diagnostic, prophylactic and therapeutic uses of BASB058 proteins, nucleic acids, and antibodies for *Neisseria meningitidis* infections.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 21 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:513807 HCAPLUS
DOCUMENT NUMBER: 133:132401
TITLE: An antigen of *Neisseria meningitidis* similar to the RlpB protein of *Escherichia coli* and its diagnostic and therapeutic uses

Searcher : Shears 308-4994

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INVENTOR(S): Thonnard, Joelle
PATENT ASSIGNEE(S): Smithkline Beecham Biologicals S.A., Belg.
SOURCE: PCT Int. Appl., 79 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000043518	A1	20000727	WO 2000-EP427	20000119
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1147194	A1	20011024	EP 2000-901585	20000119
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
PRIORITY APPLN. INFO.:			GB 1999-1465	A 19990122
			GB 1999-2077	A 19990129
			WO 2000-EP427	W 20000119

AB The invention provides *Neisseria meningitidis* BASB056 polypeptides and polynucleotides **encoding** BASB056 polypeptides and methods for producing such polypeptides by recombinant techniques. Also provided are diagnostic, prophylactic and therapeutic uses thereof. The protein was manufd. by expression of the cloned gene in *Escherichia coli*. Mice inoculated with the purified antigen mounted a strong response to it. The antigen was detectable in convalescent serum of meningitis patients.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 21 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:161171 HCAPLUS
DOCUMENT NUMBER: 132:212704
TITLE: *Neisseria gonorrhoeae* polypeptides and nucleic acid sequences for vaccines
INVENTOR(S): Jackson, W. James; Harris, Andrea M.
PATENT ASSIGNEE(S): Antex Biologics Inc., USA
SOURCE: PCT Int. Appl., 69 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000012133	A1	20000309	WO 1999-US20070	19990901
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,			

Searcher : Shears 308-4994

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IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV,
MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG,
SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE,
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
US 2002018782 A1 20020214 US 1999-388089 19990831
AU 9959066 A1 20000321 AU 1999-59066 19990901
EP 1117436 A1 20010725 EP 1999-946719 19990901
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.: US 1998-98685P P 19980901
WO 1999-US20070 W 19990901

AB The invention discloses a *Neisseria gonorrhoeae* polypeptide (NGSP), polypeptides derived therefrom (NGSP-derived polypeptides), nucleotide sequences **encoding** said polypeptides, and antibodies that specifically bind the NGSP polypeptide and/or NGSP-derived polypeptides. Also disclosed are prophylactic or therapeutic compns., including antigenic, preferably immunogenic compns., e.g. , vaccines, comprising NGSP polypeptide and/or a NGSP-derived polypeptide or antibodies thereto. The invention addnl. discloses methods of inducing an immune response to *Neisseria* and *Neisseria* NGSP polypeptide and an NGSP-derived polypeptide in animals.

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 7 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:145035 HCAPLUS

DOCUMENT NUMBER: 132:204077

TITLE: Sequence and diagnostic and prophylactic and therapeutic applications for Basb024 outer membrane protein of *Neisseria meningitidis*

INVENTOR(S): Thonnard, Joelle

PATENT ASSIGNEE(S): SmithKline Beecham Biologicals S.A., Belg.

SOURCE: PCT Int. Appl., 103 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000011182	A1	20000302	WO 1999-EP5989	19990813
W:				
AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW:				
GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9957352	A1	20000314	AU 1999-57352	19990813
EP 1105493	A1	20010613	EP 1999-944404	19990813

Searcher : Shears 308-4994

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R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.: GB 1998-18004 A 19980818
WO 1999-EP5989 W 19990813

AB The invention provides BASB024 polypeptides and polynucleotides **encoding** BASB024 polypeptides and methods for producing such polypeptides by recombinant techniques. Also provided are diagnostic, prophylactic and therapeutic uses. Serotyping is also discussed. Vaccine compns. are also described that are formulated from this BASB024 peptide.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR
THIS RECORD. ALL CITATIONS AVAILABLE IN
THE RE FORMAT

L5 ANSWER 8 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:764198 HCAPLUS

DOCUMENT NUMBER: 132:19650

TITLE: Protein and DNA sequences of Neisseria meningitidis BASB030 gene epitopes, and uses thereof in vaccine compositions and in assays for the diagnosis of bacterial infections

INVENTOR(S): Ruelle, Jean-louis

PATENT ASSIGNEE(S): Smithkline Beecham Biologicals S.A., Belg.

SOURCE: PCT Int. Appl., 96 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9961620	A2	19991202	WO 1999-EP3603	19990526
WO 9961620	A3	20000302		
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW,			
	AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
CA 2329269	AA	19991202	CA 1999-2329269	19990526
AU 9945006	A1	19991213	AU 1999-45006	19990526
EP 1080198	A2	20010307	EP 1999-927754	19990526
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, FI			
JP 2002516105	T2	20020604	JP 2000-551004	19990526
BR 9911601	A	20010206	BR 1999-11601	19991202
NO 2000005952	A	20010118	NO 2000-5952	20001124

PRIORITY APPLN. INFO.: GB 1998-11260 A 19980526
WO 1999-EP3603 W 19990526

AB The invention provides Neisseria meningitidis BASB030 polypeptides and polynucleotides **encoding** BASB030 polypeptides and methods for producing such polypeptides by recombinant techniques. Also provided are antibodies, diagnostic, prophylactic and therapeutic uses thereof. The invention also relates to the use of

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an immunogenic fragment, preferably the extracellular domain, of the provided protein in a vaccine. The invention further relates to the use of the provided protein and/or gene in the diagnosis of bacterial infections, esp. those of Neisseria.

L5 ANSWER 9 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:736937 HCAPLUS

DOCUMENT NUMBER: 131:347559

TITLE: Basb029 polynucleotide(s) and polypeptides from Neisseria meningitidis

INVENTOR(S): Ruelle, Jean-Louis

PATENT ASSIGNEE(S): Smithkline Beecham Biologicals S.A., Belg.

SOURCE: PCT Int. Appl., 74 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9958683	A2	19991118	WO 1999-EP3255	19990507
WO 9958683	A3	20000406		
W:		AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM		
RW:		GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG		
CA 2328403	AA	19991118	CA 1999-2328403	19990507
AU 9941420	A1	19991129	AU 1999-41420	19990507
EP 1078063	A2	20010228	EP 1999-924946	19990507
R:		AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, FI		
BR 9910396	A	20011030	BR 1999-10396	19990507
JP 2002514424	T2	20020521	JP 2000-548474	19990507
NO 2000005696	A	20010111	NO 2000-5696	20001110
PRIORITY APPLN. INFO.:			GB 1998-10276 A	19980513
			WO 1999-EP3255 W	19990507

AB The invention provides BASB029 polypeptides and polynucleotides **encoding** BASB029 polypeptides and methods for producing such polypeptides by recombinant techniques. Also provided are diagnostic, prophylactic and therapeutic uses as novel vaccine compns. are relayed. Prognostic and serotyping and mutation assays are all provided. In addn., antagonist and agonist screening assays are provided. Applications for immunization are relayed as well.

L5 ANSWER 10 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:708915 HCAPLUS

DOCUMENT NUMBER: 131:333044

TITLE: Protein and DNA sequences of Neisseria meningitidis BASB006 gene, and uses thereof in vaccine compositions and in assays for the diagnosis of bacterial infections

INVENTOR(S): Thonnard, Joelle

Searcher : Shears 308-4994

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PATENT ASSIGNEE(S): Smithkline Beecham Biologicals S. A., Belg.
SOURCE: PCT Int. Appl., 103 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9955873	A2	19991104	WO 1999-EP2766	19990420
WO 9955873	A3	20000309		
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
CA 2326375	AA	19991104	CA 1999-2326375	19990420
AU 9939284	A1	19991116	AU 1999-39284	19990420
EP 1071783	A2	20010131	EP 1999-922122	19990420
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
JP 2002512800	T2	20020508	JP 2000-546017	19990420
PRIORITY APPLN. INFO.:			GB 1998-8866	A 19980424
			WO 1999-EP2766	W 19990420

AB This invention provides the sequence of the Neisseria meningitidis BASB006 gene, which **encodes** a protein that has homol. to the Hap protein of Haemophilus influenzae. The invention also relates to the use of an immunogenic fragment, preferably the extracellular domain, of the provided protein in a vaccine. The invention further relates to the use of the provided protein and/or gene in the diagnosis of bacterial infections, esp. those of Neisseria.

L5 ANSWER 11 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:708914 HCAPLUS

DOCUMENT NUMBER: 131:333043

TITLE: Protein and DNA sequences of Neisseria meningitidis BASB013 gene, and uses thereof in vaccine compositions and in assays for the diagnosis of bacterial infections

INVENTOR(S): Ruelle, Jean-louis

PATENT ASSIGNEE(S): Smithkline Beecham Biologicals S.A., Belg.

SOURCE: PCT Int. Appl., 94 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9955872	A1	19991104	WO 1999-EP2765	19990420
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU,			

Searcher : Shears 308-4994

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CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV,
MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG,
SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW,
AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE,
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
CA 2326404 AA 19991104 CA 1999-2326404 19990420
AU 9938221 A1 19991116 AU 1999-38221 19990420
EP 1073747 A1 20010207 EP 1999-920767 19990420
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, FI

PRIORITY APPLN. INFO.: GB 1998-8734 A 19980423
WO 1999-EP2765 W 19990420

AB This invention provides the sequence of the Neisseria meningitidis
BASB013 gene, which **encodes** a protein that has homol. to
the MucD protein of Pseudomonas aeruginosa and to the HtrA serine
protease found in many bacteria. The invention also relates to the
use of an immunogenic fragment, preferably the extracellular domain,
of the provided protein in a vaccine. The invention further relates
to the use of the provided protein and/or gene in the diagnosis of
bacterial infections, esp. those of Neisseria.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR
THIS RECORD. ALL CITATIONS AVAILABLE IN
THE RE FORMAT

L5 ANSWER 12 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1995:583218 HCAPLUS

DOCUMENT NUMBER: 123:103932

TITLE: Nucleotide sequence and genetic variability of a
part of the rpoB gene **encoding** the
second largest subunit of DNA-directed RNA
polymerase of Neisseria meningitidis

AUTHOR(S): Nolte, Oliver

CORPORATE SOURCE: Dept. Hygiene and Microbiology, University
Heidelberg, Heidelberg, 69120, Germany

SOURCE: Med. Microbiol. Lett. (1995), 4(2), 59-67
CODEN: MMLEEH; ISSN: 1018-4627

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A PCR-generated fragment of the second largest subunit of
DNA-directed RNA polymerase (rpoB) of Neisseria meningitidis was
cloned and sequenced. Using this sequence a phylogenetic tree was
constructed. A hybridization assay performed with PCR fragments of
seven different N. meningitidis serogroups indicates genetic
differences within the genus Neisseria as well as within the species
N. meningitidis.

L5 ANSWER 13 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1992:632035 HCAPLUS

DOCUMENT NUMBER: 117:232035

TITLE: Production of outer membrane (OM) proteins in
gram-positive bacteria and recovery of
protective epitopes for vaccines

INVENTOR(S): Sarvas, Matti; Butcher, Sarah;
Nurminen-Kalliokoski, Marjatta; Runeberg-Nyman,
Kate; Mutttilainen, Susanna; Wahlstrom, Eva;

Searcher : Shears 308-4994

09/388090

PATENT ASSIGNEE(S): Idanpaan-Heikkila, Ilona; Puohiniemi, Ritvaleena
Finnish National Public Health Institute,
Finland
SOURCE: PCT Int. Appl., 42 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9201001	A1	19920123	WO 1991-FI212	19910705
W: AT, AU, BB, BG, BR, CA, CH, CS, DE, DK, ES, FI, GB, HU, JP, KP, KR, LK, LU, MC, MG, MN, MW, NL, NO, PL, RO, SD, SE, SU, US				
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GN, GR, IT, LU, ML, MR, NL, SE, SN, TD, TG				
FI 9003414	A	19920107	FI 1990-3414	19900706
CA 2086761	AA	19920107	CA 1991-2086761	19910705
AU 9181873	A1	19920204	AU 1991-81873	19910705
AU 668075	B2	19960426		
ZA 9105234	A	19930224	ZA 1991-5234	19910705
EP 538318	A1	19930428	EP 1991-912587	19910705
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
JP 06511140	T2	19941215	JP 1991-511658	19910705
AU 9660692	A1	19961107	AU 1996-60692	19960724
PRIORITY APPLN. INFO.: FI 1990-3414 19900706				
WO 1991-FI212 19910705				
AB A method is provided for producing cloned OM protein from pathogenic Gram-neg. bacteria. Also provided is a method for renaturing the cloned OM protein such that it regains immunol. active epitopes capable of eliciting antibody prodn., in mammals and other animals, that are bactericidal and can provide protection against infection by the pathogenic Gram-neg. bacteria. In the method, DNA encoding OM protein from Gram-neg. bacteria, known to be pathogenic in humans and animals, is expressed in a Gram-pos. bacterial host. The cloned OM protein produced is then renatured. Prodn. is described of cloned and renatured class 1 OM protein from Neisseria meningitidis, class 3 OM protein of N. meningitidis, and the OM protein OmpA of Escherichia coli. The cloned and renatured OM proteins are useful as vaccines. Thus, Pl.7,16 (class 1 OM protein of N. meningitidis) was cloned, then produced in Bacillus subtilis, isolated, and refolded. The presence of protective epitopes in refolded BacPl.7,16 protein was analyzed by immunizing mice and analyzing the immune sera by EIA and in bactericidal and protection assays.				

L5 ANSWER 14 OF 21 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1991:649097 HCAPLUS
DOCUMENT NUMBER: 115:249097
TITLE: Characterization of the opa (class 5) gene family of Neisseria meningitidis
AUTHOR(S): Aho, E. L.; Dempsey, J. A.; Hobbs, M. M.; Klapper, D. G.; Cannon, J. G.
CORPORATE SOURCE: Sch. Med., Univ. North Carolina, Chapel Hill, NC, 27599, USA
SOURCE: Mol. Microbiol. (1991), 5(6), 1429-37

Searcher : Shears 308-4994

CODEN: MOMIEE; ISSN: 0950-382X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Class 5 outer membrane proteins of *N. meningitidis* show both phase- and antigenic variation of expression. The proteins are **encoded** by a family of opa genes that share a conserved framework interspersed with 3 variable regions, designated the semivariable (SV) region and hypervariable regions 1 (HV1) and 2 (HV2). In this study, the no. and DNA sequence of all of the opa genes of meningococcal strain FAM18 were detd. to assess the structural and antigenic variability in the family of proteins made by 1 strain. Pulsed field electrophoresis and Southern blotting showed that there are 4 opa genes in the FAM18 chromosome, and that they are not tightly clustered. DNA sequence anal. of the 4 cloned genes showed a modest degree of diversity in the SV region and more extensive differences in the HV1 and HV2 regions. There were 4 versions of HV1 and 3 versions of HV2 among the 4 genes. Each of the FAM18 opa loci contained a gene with a unique combination of SV, HV1, and HV2 sequences. .lambda.Gt11 cloning and synthetic peptides were used to demonstrate that HV2 sequences completely **encode** the epitopes for 2 monoclonal antibodies specific for different class 5 proteins of FAM18.

L5 ANSWER 15 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1991:624918 HCAPLUS

DOCUMENT NUMBER: 115:224918

TITLE: Phase variation of gonococcal pili by frameshift mutation in pilC, a novel gene for pilus assembly

AUTHOR(S): Jonsson, Ann Beth; Nyberg, Gunilla; Normark, Staffan

CORPORATE SOURCE: Dep. Microbiol., Univ. Umea, Umea, S-90187, Swed.

SOURCE: EMBO J. (1991), 10(2), 477-88
CODEN: EMJODG; ISSN: 0261-4189

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Pili prepd. from *Neisseria gonorrhoeae* contain minor amts. of a 110 kd outer membrane protein denoted PilC. The corresponding gene exists in 2 copies, pilC1 and pilC2, in most strains of *N. gonorrhoeae*. In the piliated strain MS11(P+), only one of the genes, pilC2, was expressed. Inactivation of pilC2 by a mTnCm insertion resulted in a nonpiliated phenotype, while a mTnCm insertion in pilC1 had no effect on piliation. Expression of pilC was controlled at the translational level by frameshift mutations in a run of G residues positioned in the region **encoding** the signal peptide. Nonpiliated (P-), pilin expressing colony variants that did not express detectable levels of PilC were selected; all P+ backswitchers from these P-, PilC- clones were found to be PilC+. The structural gene for pilin, pilE, was sequenced and found to be identical in one P-, PilC- and P+, PilC+ pair. Most PilC- cells were completely bald whereas the PilC+ backswitcher had 10-40 pili per cell. Thus, a turn ON and turn OFF in the expression of PilC results in gonococcal pili phase variation. These results suggest that PilC is required for pilus assembly and/or translocation across the gonococcal outer membrane.

L5 ANSWER 16 OF 21 HCAPLUS COPYRIGHT 2002 ACS

09/388090

ACCESSION NUMBER: 1991:528653 HCAPLUS
DOCUMENT NUMBER: 115:128653
TITLE: Characterization of a gyrB mutation responsible
for low-level nalidixic acid resistance in
Neisseria gonorrhoeae
AUTHOR(S): Stein, Daniel C.; Danaher, Robert J.; Cook,
Thomas M.
CORPORATE SOURCE: Dep. Microbiol., Univ. Maryland, College Park,
MD, 20742, USA
SOURCE: Antimicrob. Agents Chemother. (1991), 35(4),
622-6
CODEN: AMACCQ; ISSN: 0066-4804
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Nalidixic acid-resistant derivs. of Neisseria gonorrhoeae WR302 were identified and categorized into two classes on the basis of their susceptibilities to this antimicrobial agent. The MIC of nalidixic acid for the deriv. strain MUG116 was fourfold greater than that for its isogenic parental strain WR302 (2 vs. 0.5 .mu.g/mL, resp.). MUG324 was significantly more resistant to nalidixic acid (>64 .mu.g/mL). The MICs of other antimicrobial agents known to interact with either the gyrA or gyrB gene products were detd. Although the nalidixic acid MIC for MUG116 increased, no significant increases in the MICs of other agents that interact with the gyrA gene product were seen. The MICs of all agents that interact with the gyrA gene product were significantly increased for MUG324. The gene that imparts low-level nalidixic acid resistance was cloned from strain MUG116. The DNA sequence of this gene was detd., and by comparing the deduced amino acid sequence with sequences of proteins in data bases, this protein was found to be .apprx.70% homologous with the gyrB gene product of Escherichia coli.

L5 ANSWER 17 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1990:605612 HCAPLUS
DOCUMENT NUMBER: 113:205612
TITLE: Molecular cloning and characterization of the
structural gene for the major iron-regulated
protein expressed by Neisseria gonorrhoeae
AUTHOR(S): Berish, Sally A.; Mietzner, Timothy A.; Mayer,
Leonard W.; Genco, Cawroline A.; Holloway, Brian
P.; Morse, Stephen A.
CORPORATE SOURCE: Cent. Infect. Dis., Cent. Dis. Control, Atlanta,
GA, 30333, USA
SOURCE: J. Exp. Med. (1990), 171(5), 1535-46
CODEN: JEMEAV; ISSN: 0022-1007
DOCUMENT TYPE: Journal
LANGUAGE: English

AB This report describes the cloning and sequencing of the major iron-regulated protein (termed Fbp) of N. gonorrhoeae strain F62. Attempts to identify recombinants expressing the Fbp using specific antibody proved unsuccessful. Therefore, an alternative cloning strategy using oligonucleotide probes derived from NH2-terminal and tryptic fragments of this protein was used to identify short fragments of the gene. Using this methodol., the gene **encoding** the precursor of Fbp was cloned on 3 sep. overlapping fragments and sequenced, and the amino acid sequence was deduced. These data were unambiguously confirmed by the known NH2-terminal amino acid sequence and were supported by the sequences

from tryptic fragments that lie outside of this region. Using oligonucleotide probes, the authors were unable to obtain clones **encoding** the potential regulatory region of this protein. Therefore, the technique of inverse polymerase chain reaction was used to amplify a fragment contg. an addnl. 200 bp. This fragment was cloned and sequenced and found to contain a consensus ribosome-binding site and potential -10 and -35 sequences. Hybridization anal. of genomic DNA from gonococcal strain F62 indicated that only a single copy of the Fbp gene exists per genome. These results complement the biochem. characterization of the Fbp expressed by gonococci and further suggest that it has a role in iron-acquisition.

L5 ANSWER 18 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1990:401205 HCAPLUS

DOCUMENT NUMBER: 113:1205

TITLE: Recombination among Protein II genes of *Neisseria gonorrhoeae* generates new coding sequences and increases structural variability in the Protein II family

AUTHOR(S): Connell, T. D.; Black, W. J.; Kawula, T. H.; Barritt, D. S.; Dempsey, J. A.; Kverneland, K., Jr.; Stephenson, A.; Schepart, B. S.; Murphy, G. L.; Cannon, J. G.

CORPORATE SOURCE: Sch. Med., Univ. North Carolina, Chapel Hill, NC, 27514, USA

SOURCE: Mol. Microbiol. (1988), 2(2), 227-36

CODEN: MOMIEE; ISSN: 0950-382X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Expression of *Neisseria gonorrhoeae* Protein II (P.II) is subject to phase variation and antigenic variation. The P.II proteins made by one strain possess both unique and conserved antigenic determinants. To study the mechanism of antigenic variation, several P.II genes were cloned using as probes a panel of monoclonal antibodies (MAbs) specific for unique determinants. The DNA sequences of three P.II genes showed that they shared a conserved framework, with 2 short hypervariable (HV) regions being responsible for most of the differences among them. Unique epitopes recognized by the MAbs were at least partially **encoded** by one of the HV regions. Moreover, reassortment of the two HV regions among P.II genes occurs, generating increased structural and antigenic variability in the P.II protein family.

L5 ANSWER 19 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1990:133318 HCAPLUS

DOCUMENT NUMBER: 112:133318

TITLE: The class 1 outer membrane protein of *Neisseria meningitidis*: gene sequence and structural and immunological similarities to gonococcal porins

AUTHOR(S): Barlow, A. K.; Heckels, J. E.; Clarke, I. N.

CORPORATE SOURCE: Med. Sch., Univ. Southampton, Southampton, SO9 4XY, UK

SOURCE: Mol. Microbiol. (1989), 3(2), 131-9

CODEN: MOMIEE; ISSN: 0950-382X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The class 1 protein is a major protein of the outer membrane of *N.*

meningitidis, and an important immunodeterminant in humans. The complete nucleotide sequence for the structural gene of a class 1 protein has been detd. The sequence predicts a protein of 374 amino acids, preceded by a typical signal peptide of 19 residues. The hydropathy profile of the predicted protein sequence resembles that of the Escherichia coli and gonococcal porins. The predicted protein sequence of the class 1 protein exhibits considerable structural similarity to the gonococcal porins PIA and PIB. Western blot studies also reveal immunol. conserved domains between the class 1 protein, PIA and PIB. A restriction fragment from the class 1 gene hybridizes to gonococcal genomic fragments in Southern blots. In addn. to the class 1 gene coding region there is a large open reading frame on the opposite strand.

L5 ANSWER 20 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1990:133280 HCAPLUS

DOCUMENT NUMBER: 112:133280

TITLE: Nucleotide sequence and genetic organization of the NgoPII restriction-modification system of Neisseria gonorrhoeae

AUTHOR(S): Sullivan, Kevin M.; Saunders, Jon R.

CORPORATE SOURCE: Dep. Genet. Microbiol., Univ. Liverpool, Liverpool, L69 3BX, UK

SOURCE: MGG, Mol. Gen. Genet. (1989), 216(2-3), 380-7
CODEN: MGGEAE; ISSN: 0026-8925

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The NgoPII restriction endonuclease, which recognizes the sequence 5'-GG.dwnarw.CC-3', differs from its isoschizomer HaeIII in being sensitive to methylation at the external cytosine residue. The entire nucleotide sequence of a cloned 3.3 kb segment of N. gonorrhoeae strain P9 chromosomal DNA which harbors the NgoPII restriction-modification system has been detd. This data, coupled with sub-cloning expts., indicates that the restriction endonuclease (R.NgoII) and modification (M.NgoII) genes are transcribed from sep. promoters but are arranged in tandem, with the R.NgoPII gene being located on the 5' side of the M.NgoPII gene. Unlike all previously reported restriction systems the 3' end of the endonuclease open reading frame overlaps the 5' end of the methylase open reading frame by 8 codons. This overlap may have implications for the regulation of the NgoPII restriction-modification system.

L5 ANSWER 21 OF 21 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1990:113019 HCAPLUS

DOCUMENT NUMBER: 112:113019

TITLE: Three copies of a single protein II-
encoding sequence in the genome of Neisseria gonorrhoeae JS3: evidence for gene conversion and gene duplication

AUTHOR(S): Van der Ley, P.

CORPORATE SOURCE: Rocky Mt. Lab., Natl. Inst. Allergy Infect. Dis., Hamilton, MT, 59840, USA

SOURCE: Mol. Microbiol. (1988), 2(6), 797-806
CODEN: MOMIEE; ISSN: 0950-382X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Gonococci express a family of related outer membrane proteins designated protein II (P.II). These surface proteins are subject to

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both phase variation and antigenic variation. The P.II gene repertoire of N. gonorrhoeae strain JS3 was found to consist of at least ten genes, eight of which were cloned. Sequence anal. and DNA hybridization studies revealed that one particular P.II-**encoding** sequence is present in three distinct, but almost identical, copies in the JS3 genome. These genes **encode** the P.II protein that was previously identified as P.IIc. Comparison of their sequences shows that the multiple copies of this P.IIc-**encoding** gene might have been generated by both gene conversion and gene duplication.

(~~FILE~~ MEDLINE, BIOSIS, EMBASE, WPIDS, JICST-EPLUS, JAPIO, CABA, AGEDSIA, VETU, VETB, PHIC, PHIN, TOXCENTER' ENTERED AT 12:25:45 ON 14 JUN 2002)

L3 197 S L2

L6 132 S L3 AND ENCOD?

L7 ~~132 S L3 AND ENCOD?~~ (81 DUPLICATES REMOVED)

L7 ANSWER 1 OF 51 WPIDS (C) 2002 THOMSON DERWENT

ACCESSION NUMBER: 2001-138654 [14] WPIDS

DOC. NO. CPI: C2001-041027

TITLE: New isolated polynucleotide useful for outer membrane vesicle preparation from Gram-negative bacterial strain for vaccination of microbial infections.

DERWENT CLASS: B04 D16

INVENTOR(S): BERTHET, F J; DALEMANS, W L J; DENOEL, P; DEQUESNE, G; FERON, C; LOBET, Y; POOLMAN, J; THIRY, G; THONNARD, J; VOET, P

PATENT ASSIGNEE(S): (SMIK) SMITHKLINE BEECHAM BIOLOGICALS

COUNTRY COUNT: 94

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

WO 2001009350	A2	20010208	(200114)*	EN	127
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC					
MW MZ NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE					
DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG					
KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ					
PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN					
YU ZA ZW					
AU 2000068336	A	20010219	(200129)		
NO 2002000506	A	20020402	(200235)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE

WO 2001009350	A2	WO 2000-EP7424	20000731
AU 2000068336	A	AU 2000-68336	20000731
NO 2002000506	A	WO 2000-EP7424	20000731
		NO 2002-506	20020131

FILING DETAILS:

Searcher : Shears 308-4994

09/388090

PATENT NO	KIND	PATENT NO
AU 2000068336	A Based on	WO 200109350

PRIORITY APPLN. INFO: GB 1999-18319 19990803

AN 2001-138654 [14] WPIDS

AB WO 200109350 A UPAB: 20010312

NOVELTY - An isolated polynucleotide sequence which hybridizes under highly stringent conditions to at least a 30 nucleotide portion of 80 sequences described in the specification.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for:

(1) a genetically-engineered outer membrane vesicle (bleb) preparation from a Gram-negative bacterial strain characterized in that the preparation is obtainable by employing a process comprising:

(a) introducing a heterologous gene, optionally controlled by a strong promoter sequence, into the chromosome by homologous recombination; and

(b) making blebs from the strain;

(2) a vaccine comprising a bleb preparation and a pharmaceutically acceptable excipient;

(3) a vector suitable for performing recombination events;

(4) a modified Gram-negative bacterial strain from which the bleb preparation is made;

(5) an immuno-protective and non-toxic Gram-negative bleb, ghost, or killed whole cell vaccine suitable for paediatric use.

ACTIVITY - Antiviral; Antibacterial; Antifungal.

Animals were immunized three times with 5 micro g of the different OMVs absorbed on Al(OH)₃ on days 0, 14, and 28. Bleedings were done on days 28 and 35, and they were challenged on day 35. The challenge dose was 20 X LD₅₀ (approx. 10 to the power of 7 CFU/mouse). Mortality rate was monitored for 7 days after challenge.

OMVs injected were:

Group1: Cps-, PorA+

Group2: Cps-, PorA-

Group3: Cps-, PorA-, NspA+

Group4: Cps-, PorA-, Omp85+

Group5: Cps-, PorA-, Hsf+

24 hours after the challenge, there was 100% mortality in the negative control group, while mice immunized with the 5 different OMVs preparations were still alive. Sickness was also monitored during the 7 days and the mice immunized with the NSPA over-expressed blebs appeared to be less sick than the other groups. PorA present in PorA+ blebs is likely to confer extensive protection against infection by the homologous strain. However, protection induced by PorA-up-regulated blebs is likely to be due at least to some extent, to the presence of increased amount of NspA, OMP85 or Hsf.

MECHANISM OF ACTION - Vaccine.

USE - The claimed polynucleotide sequence is used in performing a homologous recombination event within 1000 base pairs upstream of a Gram-negative bacterial chromosomal gene in order to either increase or decrease expression of the gene. The bleb preparation is useful in the manufacture of a medicament for immunizing a human host against a disease caused by infection of one or more of the following: *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Haemophilus influenza*, *Moraxella catarrhalis*, *Pseudomonas*

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aeruginosa, Chlamydia trachomatis, and Chlamydia pneumonia. The invention is useful for immunizing a human host against the diseases caused by the above. The invention also provides immunization against the influenza virus. Immuno-protective and non-toxic Gram-negative bleb, ghost, or killed whole cell vaccines are useful for paediatric use (all claimed).

ADVANTAGE - The vaccine is more immunogenic, less toxic, and safer.

Dwg.0/17

L7 ANSWER 2 OF 51 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-584177 [66] WPIDS
DOC. NO. CPI: C2001-173225
TITLE: Novel bacterial ribonuclease P protein useful as target in screening assays to identify compounds useful as antibacterial agents and to identify additional ribonuclease P proteins.
DERWENT CLASS: B04 D16
INVENTOR(S): EDER, P S; GIORDANO, T; GOPALAN, V; JOVANOVIC, M; POWERS, G D; XAVIER, K A
PATENT ASSIGNEE(S): (MESS-N) MESSAGE PHARM INC; (OHIS) UNIV OHIO STATE
COUNTRY COUNT: 27
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 1130091	A2	20010905	(200166)*	EN	58
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
CA 2335389	A1	20010901	(200166)	EN	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 1130091	A2	EP 2001-105007	20010301
CA 2335389	A1	CA 2001-2335389	20010301

PRIORITY APPLN. INFO: US 2000-516061 20000301

AN 2001-584177 [66] WPIDS

AB EP 1130091 A UPAB: 20011113

NOVELTY - An isolated polypeptide (I) comprising a bacterial ribonuclease P (RNase P) consensus sequence and having RNase P protein activity, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an isolated nucleic acid sequence (II) **encoding** (I);

(2) a transgenic host cell comprising (II); and

(3) an antibody that specifically binds to (I).

ACTIVITY - Antibacterial.

No supporting data is given.

MECHANISM OF ACTION - Modulator of RNase P holoenzyme activity.

USE - (I), the **protein** component of the RNase P holoenzyme is useful for identifying an antibiotic agent. The RNase P holoenzyme comprising (I) is contacted with an RNase P substrate, preferably fluorescently tagged (PtrNAGln) and the enzymatic

activity of the holoenzyme is measured by fluorescence spectroscopy. The RNase P holoenzyme comprises **Neisseria gonorrhoea** RNase P. The fluorescence analysis is carried out in a buffer comprising carbonic anhydrase (10-40 micro g/ml) and polyC (10-100 micro g/ml) and further comprises glycerol (0.5-5%), hen egg lysozyme (10-100 micro g/ml), tRNA (10-50 micro g/ml) tRNA or dithiothreitol (DTT) (1-10 mM). The enzymatic activity of the holoenzyme can also be measured by determining the fluorescence polarization level of a fluorescently tagged oligonucleotide that hybridizes to the **nucleotide** sequence cleaved by the holoenzyme or the intact substrate. A compound is identified as an antibiotic agent, if the compound produces a detectable decrease in the RNase P enzymatic activity as compared to the activity in the absence of the compound. (I) is also useful for identifying additional RNase P **nucleic** acids and **proteins**, by identifying a **nucleic** acid molecule that has sequence identity to a **nucleic** acid molecule **encoding** RNase P **polypeptide** or an amino acid molecule that has sequence identity to an RNase P **polypeptide** and determining if the amino acid molecule conserves at least nine of the 20 amino acids in Escherichia coli RNase P **protein** sequence: R11, L12, F18, R46, G48, V51, K53, K54, A59, V60, R62, N63, K66, R67, R70, L80, D84, V86, L101 and L105, where a **nucleic** acid molecule **encoding** a **polypeptide** or a **polypeptide** that does conserve at least 9 of 20 amino acids in E.coli RNase P **protein** sequence is a **polypeptide** with an RNase P consensus sequence (all claimed). The bacterial RNase P **proteins** and **polypeptides** are useful for raising antibodies which are useful for detecting RNase P **protein** in a biological sample. Compounds which modulate an RNase P holoenzyme activity are administered for treatment or prevention of a disease or condition associated with a bacterial infection.

ADVANTAGE - Inhibitors identified by (I) provide a selective antibacterial treatment that reduces the adverse side effects associated with killing nonpathogenic bacteria. Also the inhibitors reduce the risk of producing a wide range of resistant bacterial strains.

Dwg.0/3

L7 ANSWER 3 OF 51 WPIDS (C) 2002 THOMSON DERWENT
 ACCESSION NUMBER: 2001-082916 [10] WPIDS
 DOC. NO. NON-CPI: N2001-063334
 DOC. NO. CPI: C2001-024200
 TITLE: Immunogenic polypeptides derived from *Neisseria meningitidis* and the nucleic acids that **encode** them, useful for diagnosing and vaccinating against *Neisseria* infections e.g. bacteremia and meningitis.
 DERWENT CLASS: B04 D16 S03
 INVENTOR(S): NASSIF, X; TINSLEY, C; ACHTMAN, M; KLEE, S; MERKER, P
 PATENT ASSIGNEE(S): (INRM) INSERM INST NAT SANTE & RECH MEDICALE;
 (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
 COUNTRY COUNT: 95
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
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Searcher : Shears 308-4994

 EP 1069133 A1 20010117 (200110)* EN 232
 R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK
 NL PT RO SE SI
 WO 2001004150 A2 20010118 (200110) EN
 RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC
 MW MZ NL OA PT SD SE SL SZ TZ UG ZW
 W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE
 DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG
 KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ
 PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN
 YU ZA ZW
 AU 2000068254 A 20010130 (200127)
 EP 1194446 A2 20020410 (200232) EN
 R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK
 NL PT RO SE SI

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 1069133	A1	EP 1999-401764	19990713
WO 2001004150	A2	WO 2000-EP6943	20000705
AU 2000068254	A	AU 2000-68254	20000705
EP 1194446	A2	EP 2000-956222	20000705
		WO 2000-EP6943	20000705

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000068254	A Based on	WO 200104150
EP 1194446	A2 Based on	WO 200104150

PRIORITY APPLN. INFO: EP 1999-401764 19990713

AN 2001-082916 [10] WPIDS

AB EP 1069133 A UPAB: 20010220

NOVELTY - Immunologically active polypeptides (I) derived from the Gram negative bacteria *Neisseria meningitidis*, and the nucleic acids (II) that **encode** them, are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

- (1) an isolated polypeptide (I) comprising an amino acid sequence that has at least 70% identity to 44 defined amino acid sequences ((A1)-(A44)) given in the specification;
- (2) an immunogenic fragment of (I) which comprises (A1)-(A44);
- (3) an isolated polynucleotide (II) comprising a nucleotide sequence **encoding** (I) (which has at least 70% to (A1)-(A44) over its entire length), or a sequence complementary to (II);
- (4) an expression vector (III) or a recombinant live microorganism comprising (II);
- (5) a host cell (IV) comprising (III), or a membrane of (IV), that expresses a polypeptide comprising an amino acid sequence with at least 70% identity to (A1)-(A44);
- (6) a process (V) for producing a polypeptide comprising an amino acid sequence with at least 70% identity to (A1)-(A44), comprising culturing the host cell (IV) under suitable conditions

for expression of the polypeptide and recovering the polypeptide from the culture medium;

(7) a process (VI) for expressing the polynucleotide (II), comprising transforming a host cell with an expression vector comprising (II) and culturing the host cell under conditions suitable for expression of the polypeptide;

(8) vaccine compositions (VII) comprising (I) and/or (II);

(9) antibody (VIII) immuno-specific for (I); and

(10) a method for diagnosing a *Neisseria* infection, comprising identifying (I) or (VIII) in a sample from the subject animal.

ACTIVITY - Antibacterial.

MECHANISM OF ACTION - Vaccine.

Rabbit antiserum produced in response to vaccination with the polypeptides killed 65% of parenterally administered meningococcus (strain 8013) within 20 minutes of contact and all of the bacteria within 60 minutes. Pre-immune serum (taken prior to immunization) was found to have killed no bacteria after 20 minutes and only half after 60 minutes.

USE - The nucleic acids and the polypeptides they **encode** may be used to vaccinate subjects against infection by *Neisseria meningitidis* bacteria according to standard methodologies. The antibodies produced in response to the polypeptides and/or polynucleotides may also be used to treat *N. meningitidis* infections or as diagnostic reagents in immunoassays to detect infections (claimed). *N. meningitidis* is a pathogen involved in, for example, bacteremia and meningitis.
Dwg.0/50

L7 ANSWER 4 OF 51 MEDLINE DUPLICATE 1
 ACCESSION NUMBER: 2001285397 MEDLINE
 DOCUMENT NUMBER: 21116988 PubMed ID: 11179344
 TITLE: exl, an exchangeable genetic island in *Neisseria meningitidis*.
 AUTHOR: Kahler C M; Blum E; Miller Y K; Ryan D; Popovic T; Stephens D S
 CORPORATE SOURCE: Department of Medicine and Department of Microbiology and Immunology, Emory University School of Medicine, Atlanta, Georgia, USA.. charlene.kahler@monash.edu.au
 CONTRACT NUMBER: AI-33517 (NIAID)
 SOURCE: INFECTION AND IMMUNITY, (2001 Mar) 69 (3) 1687-96.
 Journal code: 0246127. ISSN: 0019-9567.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF319527; GENBANK-AF319528; GENBANK-AF319529; GENBANK-AF319530; GENBANK-AF319531; GENBANK-AF319532; GENBANK-AF319533; GENBANK-AF319534; GENBANK-AF319535; GENBANK-AF319536; GENBANK-AF319537
 ENTRY MONTH: 200105
 ENTRY DATE: Entered STN: 20010529
 Last Updated on STN: 20010529
 Entered Medline: 20010524

AB The genetic structure and evolution of a novel exchangeable meningococcal genomic island was defined for the important human pathogen *Neisseria meningitidis*. In 125 meningococcal strains tested, one of three unrelated **nucleotide** sequences, designated exl (exchangeable locus), was found between a

gene required for heme utilization, hemO, and col, **encoding** a putative Escherichia coli collagenase homologue. The 5' boundary of each ex1 cassette was the stop codon of hemO, whereas the 3' boundary was delineated by a 33-bp repeat containing **neisserial** uptake sequences located downstream of col. One of the three alternative ex1 cassettes contained the meningococcal hemoglobin receptor gene, hmbR (ex13). In other meningococcal strains, hmbR was absent from the genome and was replaced by either a **nucleotide** sequence containing a novel open reading frame, ex12, or a cassette containing ex13. The **proteins encoded** by ex12 and ex13 had no significant amino acid homology to HmbR but contained six motifs that are also present in the lipoprotein components of the lactoferrin (LbpB), transferrin (TbpB), and hemoglobin-haptoglobin (HpuA) uptake systems. To determine the evolutionary relationships among meningococci carrying hmbR, ex12, or ex13, isolates representing 92 electrophoretic types were examined. hmbR was found throughout the population structure of N. meningitidis (genetic distance, >0.425), whereas ex12 and ex13 were found in clonal groups at genetic distances of <0.2. The commensal **neisserial** species were identified as reservoirs for all of the ex1 cassettes found in meningococci. The structure of these cassettes and their correlation with clonal groups emphasize the extensive gene pool and frequent horizontal **DNA** transfer events that contribute to the evolution and virulence of N. meningitidis.

L7 ANSWER 5 OF 51 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2000:344680 BIOSIS
 DOCUMENT NUMBER: PREV200000344680
 TITLE: Hexapeptides of Neisseria gonorrhoeae.
 AUTHOR(S): Miyada, Charles Garrett (1); Born, Teresa L.
 CORPORATE SOURCE: (1) Mountain View, CA USA
 ASSIGNEE: Behringwerke Aktiengesellschaft, Marburg, Germany
 PATENT INFORMATION: US 6020461 February 01, 2000
 SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Feb. 1, 2000) Vol. 1231, No. 1, pp. No pagination. e-file.
 ISSN: 0098-1133.
 DOCUMENT TYPE: Patent
 LANGUAGE: English

AB A **nucleotide** sequence characteristic of **Neisseria gonorrhoeae** is disclosed. The sequence can be the basis for hybridization type, **nucleic acid**-based, rapid, in vitro diagnostic assays. The unique nature of the sequence makes it possible to clearly discriminate **N. gonorrhoeae** from other **Neisseria** species thus eliminating or substantially reducing the number of false positive readings. A 350 base pair **N. gonorrhoeae DNA** restriction fragment was cloned after subtractive hybridization to **Neisseria meningitidis DNA**. In further cloning experiments the sequences adjacent to the original 350 base pair fragment were determined. A portion of this sequence was shown to detect 105 of 106 **N. gonorrhoeae** strains and no other **Neisseria** species. In addition to use as detection probes, all or portions of the **nucleotide** sequence can be used as a ligand for the sandwich capture of **N. gonorrhoeae** sequences and as primers for in vitro

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amplification of *N. gonorrhoeae* sequences. The polypeptides encoded by the presently disclosed sequence, including antibodies thereto, are also disclosed as are their uses.

L7 ANSWER 6 OF 51 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2000-647603 [62] WPIDS
CROSS REFERENCE: 2000-062150 [01]; 2000-318079 [27]; 2001-557776 [58]; 2001-582163 [58]
DOC. NO. CPI: C2000-195957
TITLE: Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections.
DERWENT CLASS: B04 D16
INVENTOR(S): FRAZER, C M; GALEOTTI, C; GRANDI, G; HICKEY, E; MASIGNANI, V; MORA, M; PETERSON, J; PIZZA, M; RAPPUOLI, R; RATTI, G; SCARLATO, V; SCARSELLI, M; TETTELIN, H; VENTER, J C
PATENT ASSIGNEE(S): (CHIR) CHIRON CORP; (GENO-N) INST GENOMIC RES
COUNTRY COUNT: 92
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

WO 2000066791	A1	20001109	(200062)*	EN	669
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000032492	A	20001117	(200111)		
EP 1185691	A1	20020313	(200225)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE

WO 2000066791	A1	WO 2000-US5928	20000308
AU 2000032492	A	AU 2000-32492	20000308
EP 1185691	A1	EP 2000-910392	20000308
		WO 2000-US5928	20000308

FILING DETAILS:

PATENT NO	KIND	PATENT NO

AU 2000032492	A Based on	WO 200066791
EP 1185691	A1 Based on	WO 200066791

PRIORITY APPLN. INFO: GB 2000-4695 20000228; US 1999-132068P 19990430; WO 1999-US23573 19991008

AN 2000-647603 [62] WPIDS
CR 2000-062150 [01]; 2000-318079 [27]; 2001-557776 [58]; 2001-582163 [58]
AB WO 200066791 A UPAB: 20020418
NOVELTY - A nucleic acid (I) comprising the full length genome of

Searcher : Shears 308-4994

Neisseria meningitidis B (NMB) (II) or one or more NMB open reading frames, all given in the specification, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

- (1) a method for identifying an amino acid (aa) sequence comprising searching for putative open reading frames or protein coding sequences within (I);
- (2) a method for producing a protein comprising expressing a protein comprising an aa sequence identified by the above method;
- (3) a method for identifying a protein in *N. meningitidis* comprising producing a protein as in (2), producing an antibody which binds to the protein and determining whether the antibody recognizes a protein produced by *N. meningitidis*;
- (4) nucleic acid comprising an open reading frame or protein coding sequence identified by the method of (1);
- (5) a protein (V) obtained by the method of (2);
- (6) a nucleic acid (II) comprising a fragment of (I);
- (7) a nucleic acid (III) comprising a nucleotide sequence with greater than 50% sequence identity to (I);
- (8) a nucleic acid complementary to (I), (II) or (III);
- (9) a protein (VI) comprising an aa sequence **encoded** within (I);
- (10) a protein (VII) comprising an aa sequence having greater than 50% sequence identity to an aa sequence **encoded** within (I);
- (11) a protein (VIII) comprising a fragment of an aa sequence **encoded** within (I);
- (12) nucleic acid (IV) **encoding** one of (VI)-(VIII);
- (13) a computer, a computer memory, a computer storage medium or a computer database containing (I), (II) or (III);
- (14) a polyclonal or monoclonal antibody which binds to (VI)-(VIII) or (V);
- (15) a nucleic acid probe comprising nucleic acid (I), (II), (III) or (IV); and
- (16) an amplification primer comprising nucleic acid (I), (II), (III) or (IV).

ACTIVITY - Antibacterial.

No biological data is given.

MECHANISM OF ACTION - Vaccine; Gene therapy.

USE - Nucleic acids (I), (II), (III) or (IV), protein (VI)-(VIII) or (V) and/or antibody which binds to (VI)-(VIII) or (V) can be used in a composition for treating or preventing infection due to *Neisserial* bacteria or as a diagnostic reagent for detecting the presence of *Neisserial* bacteria or of antibodies raised to *Neisserial* bacteria (claimed).

The computer, computer memory, computer storage medium or computer database can be used in a search to identify open reading frames (ORFs) or coding sequences within (I).

ADVANTAGE - The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used.

Dwg.0/18

L7 ANSWER 7 OF 51 WPIDS (C) 2002 THOMSON DERWENT
 ACCESSION NUMBER: 2000-423415 [36] WPIDS
 DOC. NO. CPI: C2000-128234
 TITLE: Isolated nucleic acid molecule for eliciting immune response in mammal **encodes** *Neisseria*

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meningitidis heat shock protein 70, Aspergillus
fumigatus Hsp60 and Candida glabrata Hsp60
polypeptide.
DERWENT CLASS: B04 D16
INVENTOR(S): WISNIEWSKI, J
PATENT ASSIGNEE(S): (STRE-N) STRESSGEN BIOTECHNOLOGIES CORP
COUNTRY COUNT: 90
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000034465	A2	20000615	(200036)*	EN	118
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC					
MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM					
EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ					
LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU					
SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW					
AU 2000015408	A	20000626	(200045)		
EP 1137770	A2	20011004	(200158)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK					
NL PT RO SE SI					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000034465	A2	WO 1999-CA1152	19991201
AU 2000015408	A	AU 2000-15408	19991201
EP 1137770	A2	EP 1999-957790	19991201
		WO 1999-CA1152	19991201

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000015408	A Based on	WO 200034465
EP 1137770	A2 Based on	WO 200034465

PRIORITY APPLN. INFO: US 1998-207388 19981208

AN 2000-423415 [36] WPIDS

AB WO 200034465 A UPAB: 20000801

NOVELTY - An isolated nucleic acid molecule **encoding**
Neisseria meningitidis heat shock protein (Hsp) 70 (I), Aspergillus
fumigatus Hsp60 (II) or Candida glabrata Hsp60 (III) polypeptide, is
new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for
the following:

(1) an isolated nucleic acid selected from a 2465, 1929 or 1989
base pair sequence, nucleotides 357-2286 of the 2465 base pair
sequence (bps), or nucleotides 4-1932 of a 1932 bps, all fully
defined in the specification, and their complements;

(2) an isolated nucleic acid molecule comprising a nucleotide
sequence identical to a segment of contiguous nucleotide bases
comprising at least 25% of a 2465 bps at position 358-2286, a 1932
bps, a 1929 bps or 1989 bps or a complement;

(3) an isolated nucleic acid molecule comprising a nucleotide
sequence identical to the segment of contiguous nucleotide bases

comprising at least 25% of a 2480 bps, a 1761 bps, or a 1820 bps, all fully defined in the specification, or a complement;

(4) an isolated nucleic acid molecule comprising a nucleotide sequence identical to the segment of contiguous nucleotide bases comprising at least 25% of a 2051 bps, a 1755 bps or a 1814 bps, all fully defined in the specification, or a complement;

(5) isolated nucleic acid molecule comprising a nucleic acid sequence that **encodes** a polypeptide comprising a 1005, 2465, 1932, 1929, or 1981 bps, all fully defined in the specification, or a variant Hsp70 that is at least 95% homologous to the polypeptide, percentage homology is determined to an algorithm incorporated in a protein database search program used in BLAST (RTM) or DNA star Megalign (RTM);

(6) isolated nucleic acid molecule comprising a nucleic acid sequence that **encodes** a polypeptide comprising a 2480, 1761, or 1820 bps, ally fully defined in the specification, or a variant Hsp60 that is at least 95% homologous to the polypeptide, percentage homology is determined to an algorithm incorporated in a protein database search program used in BLAST (RTM) or DNA star Megalign (RTM);

(7) isolated nucleic acid molecule comprising a nucleic acid sequence that **encodes** a polypeptide comprising a 2051, 1755, or 1814 bps, all fully defined in the specification, or a variant Hsp60 that is at least 95% homologous to the polypeptide, percentage homology is determined to an algorithm incorporated in a protein database search program used in BLAST (RTM) or DNA star Megalign (RTM);

(8) isolated nucleic acid molecule **encoding** at least 8 contiguous amino acids of (I) from the 1932 base pair sequence, where the **encoded** polypeptide is able to bind to a major histocompatibility complex;

(9) isolated nucleic acid molecule **encoding** at least 8 contiguous amino acids of (II) from the 2480 base pair sequence, where the **encoded** polypeptide is able to bind to a major histocompatibility complex;

(10) isolated nucleic acid molecule **encoding** at least 8 contiguous amino acids of (III) from the 2051 base pair sequence, where the **encoded** polypeptide is able to bind to a major histocompatibility complex;

(11) isolated (I), (II) and (III);

(12) isolated polypeptide comprising an amino acid sequence having at least 95% homology to the polypeptide with a 641, 585, or 561 residue amino acid sequence, fully defined in the specification, which selectively binds to an antibody specific for (I), (II), or (III) respectively;

(13) a vector (V) containing the isolated nucleic acid molecule **encoding** (I), (II) or (III);

(14) host cell containing (V);

(15) composition comprising (I), (II) or (III) in combination with a carrier or diluent; and

(16) a probe or polymerase chain reaction (PCR) primer (P) for detecting DNA **encoding** (I), comprising at least 15 contiguous bases from a 2465, 1932, 1929 or 1981 base pair sequence, (II) comprising at least 15 contiguous bases from a 2480, 1761 or 1820 base pair sequence and (III), comprising at least 15 contiguous bases from a 2051, 1755, 1814 base pair sequence.

ACTIVITY - Antibiotic.

MECHANISM OF ACTION - The polypeptides generate an immune

response to the bacteria.

USE - (I), (II) and (III) are useful for eliciting or enhancing an immune response in a mammal against **Neisseria meningitidis**, **Candida glabrata** and **Aspergillus fumigatus**, by administering target antigen joined to (I), (II) or (III) **polypeptide**, or a fusion **protein** containing sequences of the **polypeptide** fused to sequences of (I), (II) or (III) **polypeptide** (claimed). They are useful for diagnosing the presence of (I), (II) or (III) in a sample by performing a polymerase chain reaction (PCR) amplification of **DNA** fraction obtained from the sample using at least one (P) (claimed). (I), (II) or (III) **nucleotide** sequences are useful for producing recombinant **proteins** for immunizing an animal.

Dwg.0/27

L7 ANSWER 8 OF 51 WPIDS (C) 2002 THOMSON DERWENT
 ACCESSION NUMBER: 2000-271267 [23] WPIDS
 DOC. NO. CPI: C2000-082777
 TITLE: New antisense oligonucleotide, useful for treating and diagnosing bacterial infections, interacts with and inhibits translation of a target RNA sequence in bacteria.
 DERWENT CLASS: B04 D16
 INVENTOR(S): SEIFERT, W
 PATENT ASSIGNEE(S): (VITA-N) VITAGENIX INC
 COUNTRY COUNT: 89
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000015265	A1	20000323	(200023)*	EN	47
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC					
MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM					
EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ					
LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD					
SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
AU 9962589	A	20000403	(200034)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000015265	A1	WO 1999-US21950	19990915
AU 9962589	A	AU 1999-62589	19990915

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9962589	A Based on	WO 200015265

PRIORITY APPLN. INFO: US 1998-100625P 19980916; US 1998-100591P 19980916; US 1998-100598P 19980916; US 1998-100599P 19980916

AN 2000-271267 [23] WPIDS
 AB WO 200015265 A UPAB: 20000516

NOVELTY - An antisense oligonucleotide (I) which interacts with and inhibits translation of a target RNA sequence in a bacteria, where the target RNA **encodes** a protein such as enzymes for biosynthesis of cell wall proteins, ribosomal RNA, ribosomal proteins, proteins essential for nutrient uptake, proteins associated with pathogenicity, subunits of DNA-dependent RNA polymerase and DNA polymerase, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method for inhibiting a disease associated with a bacterial infection, comprises administering a composition comprising (I);

(2) a method of inhibiting bacterial cell growth and pathogenesis, comprises contacting a sample with an inhibiting amount of (I);

(3) a chimeric antisense (II) oligonucleotide, comprising an antisense oligonucleotide linked to an uptake sequence; and

(4) a diagnostic method of determining the presence of bacteria in a sample, comprising contacting the sample with an uptake sequence linked to a reporter construct.

ACTIVITY - Antibacterial.

MECHANISM OF ACTION - The antisense oligonucleotides interact with and inhibits translation of a target RNA sequence in a bacteria.

USE - (I) and (II) are useful in treating or diagnosing bacterial infections.

Dwg.0/1

L7 ANSWER 9 OF 51 WPIDS (C) 2002 THOMSON DERWENT
 ACCESSION NUMBER: 2000-533868 [49] WPIDS
 DOC. NO. CPI: C2000-159308
 TITLE: Host cell, useful e.g. as bioreactor for production of poly(hydroxyalkanoate), containing two or more recombinant polypeptides, with at least one in carrier-bound form.
 DERWENT CLASS: B04 D16
 INVENTOR(S): LUBITZ, W
 PATENT ASSIGNEE(S): (LUBI-I) LUBITZ W
 COUNTRY COUNT: 91
 PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
DE 19903345	A1	20000803	(200049) *		25
WO 2000044878	A1	20000803	(200049)	GE	
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC					
MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM					
EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ					
LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU					
SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000026675	A	20000818	(200057)		
EP 1144590	A1	20011017	(200169)	GE	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK					
NL PT RO SE SI					

APPLICATION DETAILS:

09/388090

PATENT NO	KIND	APPLICATION	DATE
DE 19903345	A1	DE 1999-19903345	19990128
WO 2000044878	A1	WO 2000-EP686	20000128
AU 2000026675	A	AU 2000-26675	20000128
EP 1144590	A1	EP 2000-904978	20000128
		WO 2000-EP686	20000128

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000026675	A Based on	WO 200044878
EP 1144590	A1 Based on	WO 200044878

PRIORITY APPLN. INFO: DE 1999-19903345 19990128

AN 2000-533868 [49] WPIDS

AB DE 19903345 A UPAB: 20001006

NOVELTY - Host cell (A) comprising at least two functional recombinant polypeptides (I), at least one being in carrier bound form, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

- (1) recombinant bacterial ghosts (B) produced from (A); and
- (2) method for preparing (A).

ACTIVITY - Antibacterial.

MECHANISM OF ACTION - Vaccine

No biological data given.

USE - (A), or, where bacterial, their ghosts (B), are useful as vaccines or adjuvants (specifically for presentation of immunogenic epitopes of pathogens or autologous immunostimulatory polypeptides, e.g. cytokines), or preferably, as enzyme reactors for performing a cascade of reactions, specifically synthesis of poly(hydroxyalkanoate).

ADVANTAGE - Localization of individual (I), specifically enzymes, in separate cellular compartments avoids adverse reactions between products and substrates, when being used as bioreactors. (I) can be produced in carrier-bound form without loss of function.
Dwg.0/2

L7 ANSWER 10 OF 51 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2000157034 MEDLINE
DOCUMENT NUMBER: 20157034 PubMed ID: 10655208
TITLE: A homologue of the recombination-dependent growth gene, rdgC, is involved in gonococcal pilin antigenic variation.
AUTHOR: Mehr I J; Long C D; Serkin C D; Seifert H S
CORPORATE SOURCE: Department of Microbiology-Immunology, Northwestern University Medical School, Chicago, Illinois 60611, USA.
CONTRACT NUMBER: R01 AI33493 (NIAID)
T32 AI07476 (NIAID)
T32 GM08061 (NIGMS)
SOURCE: GENETICS, (2000 Feb) 154 (2) 523-32.
Journal code: 0374636. ISSN: 0016-6731.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

Searcher : Shears 308-4994

09/388090

FILE SEGMENT: Priority Journals
ENTRY MONTH: 200003
ENTRY DATE: Entered STN: 20000327
Last Updated on STN: 20000327
Entered Medline: 20000314

AB *Neisseria gonorrhoeae* pilin undergoes high-frequency changes in primary amino acid sequence that aid in the avoidance of the host immune response and alter pilus expression. The pilin amino acid changes reflect **nucleotide** changes in the expressed gene, *pilE*, which result from nonreciprocal recombination reactions with numerous silent loci, *pilS*. A series of mini-transposon insertions affecting pilin antigenic variation were localized to three genes in one region of the Gc chromosome. Mutational analysis with complementation showed that a Gc gene with sequence similarity to the *Escherichia coli* *rdgC* gene is involved in pilus-dependent colony phase variation and in pilin antigenic variation. Furthermore, we show that the Gc *rdgC* homologue is transcriptionally linked in an operon with a gene **encoding** a predicted GTPase. The inability to disrupt expression of this gene suggests it is an essential gene (*engA*, essential **neisserial** GTPase). While some of the transposon mutations in *rdgC* and insertions in the 5'-untranslated portion of *engA* showed a growth defect, all transposon insertions investigated conferred an aberrant cellular morphology. Complementation analysis showed that the growth deficiencies are due to the interruption of *RdgC* expression and not that of *EngA*. The requirement of *RdgC* for efficient pilin variation suggests a role for this **protein** in specialized **DNA** recombination reactions.

L7 ANSWER 11 OF 51 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1999412224 MEDLINE
DOCUMENT NUMBER: 99412224 PubMed ID: 10481080
TITLE: Identification of a virulence-associated protein homolog gene and *ISRa1* in a plasmid of *Riemerella anatipestifer*.
AUTHOR: Weng S; Lin W; Chang Y; Chang C
CORPORATE SOURCE: Department of Veterinary Medicine, National Taiwan University, 142 Chou San Road, Taipei, Taiwan.
SOURCE: FEMS MICROBIOLOGY LETTERS, (1999 Oct 1) 179 (1) 11-9.
Journal code: 7705721. ISSN: 0378-1097.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF082180
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991104

AB *Riemerella anatipestifer* is the causative agent of polyserositis of ducks and geese. We have previously reported that a 3.9-kb plasmid, *pCFC1*, carries **protein** genes (*vapD1* and *vapD2*) that are similar to virulence-associated genes of other bacteria. In the present study, we report the complete sequence of a second plasmid of 5.6 kb, *pCFC2*. *pCFC2* has a 28% G-C content and three large open reading frames (ORFs). One of the ORFs (designated as *VapD1*) **encodes a polypeptide** that shares 53.9, 53.9, 48.3, 48.3 and 46.1% identity with virulence-associated

proteins of *Dichelobacter nodosus*, *Actinobacillus actinomycetemcomitans*, *Neisseria gonorrhoeae*, *Helicobacter pylori* and *Haemophilus influenzae*, respectively. The second ORF **encodes** a putative **DNA** replication **protein** (RepA3) with 309 amino acids and a molecular mass of approximately 36 kDa. A novel insertion sequence (IS) element, designated ISRa1, was found on the plasmid pCFC2. ISRa1 was flanked by 15-bp imperfect inverted repeats (only one mismatched **nucleotide**). ISRa1 contained an ORF **encoding** a putative transposase of 292 amino acids. Southern blot analysis indicated that in *R. anatipestifer* strains examined, ISRa1 was present with 2-20 copies (at least). ISRa1 displayed a sequence approximately 35% homologous to the putative IS982 and RSBst- α from *Lactococcus lactis* ssp. *cremoris* SK11 and *Bacillus stearothermophilus* CU21. Three hybridization patterns of genomic **DNA** of eight *R. anatipestifer* strains with an ISRa1 probe indicated that ISRa1 might be a useful tool for epidemiological studies.

L7 ANSWER 12 OF 51 MEDLINE DUPLICATE 4
 ACCESSION NUMBER: 1999354439 MEDLINE
 DOCUMENT NUMBER: 99354439 PubMed ID: 10425707
 TITLE: The neisserial 37 kDa ferric binding protein (FbpA).
 AUTHOR: Ferreiros C; Criado M T; Gomez J A
 CORPORATE SOURCE: Departamento de Microbiologia y Parasitologia,
 Facultad de Farmacia, Universidad de Santiago de
 Compostela, Spain.. mpcfytc@usc.es
 SOURCE: COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY. PART B,
 BIOCHEMISTRY AND MOLECULAR BIOLOGY, (1999 May) 123
 (1) 1-7. Ref: 53
 Journal code: 9516061. ISSN: 1096-4959.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199911
 ENTRY DATE: Entered STN: 20000111
 Last Updated on STN: 20000111
 Entered Medline: 19991103

AB The ferric binding **protein** (FbpA) is one of the major **proteins** regulated by the level of environmental iron in the genus *Neisseria*. Its conservation in all species of pathogenic *Neisseria* has been demonstrated, and the possible role that it plays in the iron uptake mechanisms in these bacteria has been postulated. Similar **proteins** in *Haemophilus influenzae* (HitA) and in *Serratia marcescens* (SfuA) have been described, but relationships with the meningococcal FbpA could not be proven. Although supposedly periplasmic, the exact location of FbpA remains controversial because some molecules, or parts of them, have been found exposed to the bacterial outer surface. The **DNA** sequence downstream of the fbpA gene has been recently analysed, finding an operon composed of three open reading frames: fbpA, **encoding** for FbpA; fbpB, that codifies a cytoplasmic permease, and fbpC, that contains the information for a **nucleotide** binding **protein**. These **proteins** would form an iron transport system through the periplasmic space.

FbpA is highly antigenic in mice when injected in purified form, shows intraspecies and interspecies antigenic homogeneity, and specific anti-FbpA antibodies are fully cross-reactive; nevertheless, the in vivo induction of anti-FbpA antibodies in man is still polemical. Recent studies reveal that the purified FbpA induces a fair response of bactericidal antibodies in mice.

L7 ANSWER 13 OF 51 MEDLINE DUPLICATE 5
 ACCESSION NUMBER: 1999098704 MEDLINE
 DOCUMENT NUMBER: 99098704 PubMed ID: 9884235
 TITLE: The Pasteurella haemolytica 35 kDa iron-regulated protein is an FbpA homologue.
 AUTHOR: Kirby S D; Lainson F A; Donachie W; Okabe A; Tokuda M; Hatase O; Schryvers A B
 CORPORATE SOURCE: Department of Microbiology and Infectious Diseases, University of Calgary, Alberta, Canada..
 SOURCE: sdkirby@acs.ucalgary.ca
 MICROBIOLOGY, (1998 Dec) 144 (Pt 12) 3425-36.
 Journal code: 9430468. ISSN: 1350-0872.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF047427
 ENTRY MONTH: 199904
 ENTRY DATE: Entered STN: 19990511
 Last Updated on STN: 19990511
 Entered Medline: 19990429

AB In a previous investigation, a 35 kDa iron-regulated **protein** was identified from total cellular **proteins** of Pasteurella haemolytica grown under iron-depleted conditions. This study reports identification of the gene (fbpA) **encoding** the 35 kDa **protein** based on complementation of an entA Escherichia coli strain transformed with a plasmid derived from a P. haemolytica lambda ZAP II library. Cross-reactivity was demonstrated between an anti-35 kDa mAb and a 35 kDa **protein** expressed in this strain. Furthermore, a translated ORF identified on the recombinant plasmid corresponded with the N-terminal amino acid sequence of the intact and a CNBr-cleaved fragment of the 35 kDa iron-regulated **protein**. Nucleotide sequence analysis of the gene **encoding** the 35 kDa **protein** demonstrated homology with the cluster 1 group of extracellular solute-binding **proteins**, especially to the iron-binding **proteins** of this family. Complete sequence analysis of the recombinant plasmid insert identified three other predominant ORFs, two of which appeared to be in an operonic organization with fbpA. These latter components (fbpB and fbpC) showed homology to the transmembrane and ATPase components of ATP-binding cassette (ABC)-type uptake systems, respectively. Based on amino acid/DNA sequencing, citrate competition assay of iron affinity and visible wavelength spectra, it was concluded that the P. haemolytica 35 kDa **protein** functions as an FbpA homologue (referred to as PFbpA) and that the gene **encoding** this **protein** is part of an operon comprising a member of the FbpABC family of iron uptake systems. Primary sequence analysis revealed rather surprisingly that PFbpA is more closely related to the intracellular Mn/Fe-binding **protein** IdIA found in cyanobacteria than to any of the homologous FbpA **proteins** currently known in commensal or

pathogenic members of the Pasteurellaceae or **Neisseriaceae**

L7 ANSWER 14 OF 51 MEDLINE DUPLICATE 6
 ACCESSION NUMBER: 1998234299 MEDLINE
 DOCUMENT NUMBER: 98234299 PubMed ID: 9565669
 TITLE: Characterization of the region downstream of the pilus biogenesis gene pilC1 in *Neisseria gonorrhoeae*.
 AUTHOR: Kallstrom H; Jonsson A B
 CORPORATE SOURCE: Microbiology and Tumorbiology Center, Karolinska Institute, Box 280, 171 77 Stockholm, Sweden.
 SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (1998 Apr 29) 1397 (2) 137-40.
 Journal code: 0217513. ISSN: 0006-3002.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ002423
 ENTRY MONTH: 199806
 ENTRY DATE: Entered STN: 19980611
 Last Updated on STN: 19980611
 Entered Medline: 19980601

AB The **nucleotide** sequence of a 3 kb region downstream of pilC1 in ***Neisseria gonorrhoeae*** MS11 was analyzed. This region contains two open reading frames, ORF1 and ORF2, and several repetitive **DNA** elements. ORF1 **encodes** an outer membrane **protein** that shows homology to orf98 of *Pedococcus acidilactici*. PCR with primers specific for ORF1 revealed that the gene is present in all gonococcal strains tested. The other open reading frame, ORF2, is highly homologous to the putative integral membrane **protein** HI1680 of *Haemophilus influenzae*.
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L7 ANSWER 15 OF 51 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1998:256290 BIOSIS
 DOCUMENT NUMBER: PREV199800256290
 TITLE: Characterization of the region downstream of the pilus biogenesis gene pilC1 in *Neisseria gonorrhoeae*.
 AUTHOR(S): Kallstrom, Helena; Jonsson, Ann-Beth (1)
 CORPORATE SOURCE: (1) Microbiol. and Tumorbior. Cent., Karolinska Inst., Box 280, 171 77 Stockholm Sweden
 SOURCE: Biochimica et Biophysica Acta, (April 29, 1998) Vol. 139, No. 2, pp. 137-140.
 ISSN: 0006-3002.
 DOCUMENT TYPE: Article
 LANGUAGE: English

AB The **nucleotide** sequence of a 3 kb region downstream of pilC1 in ***Neisseria gonorrhoeae*** MS11 was analyzed. This region contains two open reading frames, ORF1 and ORF2, and several repetitive **DNA** elements. ORF1 **encodes** an outer membrane **protein** that shows homology to orf98 of *Pedococcus acidilactici*. PCR with primers specific for ORF1 revealed that the gene is present in all gonococcal strains tested. The other open reading frame, ORF2, is highly homologous to the putative integral membrane **protein** HI1680 of *Haemophilus influenzae*.

09/388090

L7 ANSWER 16 OF 51 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 1997-180942 [17] WPIDS
DOC. NO. NON-CPI: N1997-148829
DOC. NO. CPI: C1997-058488
TITLE: Nucleic acids **encoding** Neisseria adhesion
proteins - for therapeutic and diagnostic use.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): EICKERNJAEGER, S; FISCHER, E; MAIER, J; MEYER, T;
RUDEL, T; SCHEUERPFUG, I; SCHWAN, T; MEYER, T F
PATENT ASSIGNEE(S): (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
COUNTRY COUNT: 20
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
DE 19534579	A1	19970320	(199717)*		20
WO 9711181	A1	19970327	(199718)	GE	60
RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: JP US					
EP 852623	A1	19980715	(199832)	GE	
R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
DE 19534579	C2	20000608	(200032)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
DE 19534579	A1	DE 1995-19534579	19950918
WO 9711181	A1	WO 1996-EP4092	19960918
EP 852623	A1	EP 1996-932563	19960918
		WO 1996-EP4092	19960918
DE 19534579	C2	DE 1995-19534579	19950918

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 852623	A1 Based on	WO 9711181

PRIORITY APPLN. INFO: DE 1995-19534579 19950918

AN 1997-180942 [17] WPIDS

AB DE 19534579 A UPAB: 19970424

A novel **nucleic** acid mol. (I) where the open reading frame **encodes Neisseria proteins** that mediate adhesion of **Neisseria** cells to human cells is selected from the group of: (i) a **nucleic** acid mol. with a 3287 bp (given in the specification); (ii) a **nucleic** acid mol. as in (i) within the degeneracy of the genetic codon; and (iii) a **nucleic** acid mol. which hybridises with (i) or (ii). Also claimed are: (1) **nucleic** acid mols. (Ia), (Ib) and (Ic) which are fragments of (I) as above, that **encode** lipoprotein (OrfA, I and B resp.), selected from the group of: (i) **nucleic** acid mols. **encoding** a 320 (esp. residues 19-320), 104 or 509 amino acid residue sequence; (ii) **nucleic** acid mols. comprising **nucleotides** 189-1095 of a 1136 bp sequence (Ia), a 582 bp (Ib) and a 1744 bp (Ic) sequence; (iii) **nucleic** acid mols. as in (i) or (ii)

within the degeneracy of the genetic codon; and (iv) a **nucleic acid** mol. which hybridises with (i), (ii) or (iii); (2) vectors contg. the **nucleic acids** of (1); (3) host cells contg. the vectors; (4) **proteins encoded** by the **nucleic acids** of (1); (5) antibodies to the **proteins** of (4); (6) cell receptors that bind to OrfA and inhibit its adhesion function; (7) receptor analogues that modulate the adhesion function of OrfA by acting as competitive inhibitors; and (8) inhibitors that inhibit the interaction between OrfA and cell receptors.

USE - The products are useful in medicaments, diagnostic compsns. and vaccines (claimed), esp. for treatment of *Neisseria gonorrhoea* and *N. meningitidis* infections.
Dwg.0/1

L7 ANSWER 17 OF 51 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
DUPLICATE 7

ACCESSION NUMBER: 1997:515443 BIOSIS

DOCUMENT NUMBER: PREV199799814646

TITLE: Phase variation and conservation of

AUTHOR(S): lipooligosaccharide epitopes in *Haemophilus somnus*.
Inzana, Thomas J. (1); Hensley, Jennifer; McQuiston, John; Lesse, Alan J.; Campagnari, Anthony A.; Boyle, Stephen M.; Apicella, Michael A.

CORPORATE SOURCE: (1) Cent. Mol. Med. Infect. Dis., Virginia-Maryland
Regional Coll. Vet. Med., Virginia Polytechnic Inst.
State Univ., Blacksburg, VA USA

SOURCE: Infection and Immunity, (1997) Vol. 65, No. 11, pp.
4675-4681.
ISSN: 0019-9567.

DOCUMENT TYPE: Article

LANGUAGE: English

AB The bovine-specific pathogen *Haemophilus somnus* is capable of undergoing structural and antigenic phase variation in its lipooligosaccharide (LOS) components after in vivo and in vitro passage. However, commensal isolates from the reproductive tract have not been observed to vary in phase (T. J. Inzana, R. P. Gogolewski, and L. B. Corbeil, *Infect. Immun.* 60:2943-2951, 1992). We now report that specific monoclonal antibodies (MAbs) to the LOSs of *Haemophilus aegyptius*, *Neisseria gonorrhoeae*, and *Haemophilus influenzae*, as well as *H. somnus*, reacted with some phase-variable epitopes in *H. somnus* LOS. All reactive MAbs bound to LOS components of about 4.3 kDa in the same *H. somnus* isolates, including a non-phase-varying strain. Following in vitro passage of a clonal variant of strain 738 that was nonreactive with the MAbs, 11.8% of young colonies shifted to a reactive phenotype. A digoxigenin-labelled 5'-CAATCAATCAATCAATCAATCAATCAAT-3' oligo-**nucleotide** probe hybridized to genomic **DNA** from strain 738 but did not react with **DNA** from a non-phase-varying strain. Sequence analysis of the gene containing 5'-CAAT-3' tandem sequences revealed 48% amino acid homology with the lex-2B gene-**encoded protein** of *H. influenzae* type b. Our results indicate that some LOS epitopes are conserved between *H. somnus* and other *Haemophilus* and *Neisseria* species, that LOS phase variation may occur at a high rate in some strains of *H. somnus*, and that phase variation may, in part, be due to 5'-CAAT-3' tandem sequences present in *H. somnus* genes.

L7 ANSWER 18 OF 51 MEDLINE DUPLICATE 8
 ACCESSION NUMBER: 97285757 MEDLINE
 DOCUMENT NUMBER: 97285757 PubMed ID: 9140974
 TITLE: Cloning and functional characterization of *Neisseria gonorrhoeae* tonB, exbB and exbD genes.
 AUTHOR: Biswas G D; Anderson J E; Sparling P F
 CORPORATE SOURCE: Department of Medicine, University of North Carolina, Chapel Hill 27599, USA.
 CONTRACT NUMBER: AI-26837 (NIAID)
 AI-31496 (NIAID)
 SOURCE: MOLECULAR MICROBIOLOGY, (1997 Apr) 24 (1) 169-79.
 Journal code: 8712028. ISSN: 0950-382X.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U79563
 ENTRY MONTH: 199707
 ENTRY DATE: Entered STN: 19970812
 Last Updated on STN: 19970812
 Entered Medline: 19970728

AB ***Neisseria gonorrhoeae*** is able to utilize iron (Fe) from a variety of sources including transferrin (TF) and lactoferrin (LF). To gain insight into the molecular mechanisms used by gonococci to scavenge Fe from TF and LF, we cloned a 3.5 kb segment of wild-type DNA that repaired the defect in *tlu* mutants, which are unable to take up Fe from either TF or LF despite exhibiting apparently normal ligand binding to the receptor. Nucleotide sequence determination identified three open reading frames (ORFs), designated ORF1, ORF2, and ORF3, which were arranged in tandem. The deduced amino acid sequence of the 852 bp ORF1 encoded a 28 kDa protein that exhibited 26-32% identity with TonB proteins of nine other bacteria. The 663 bp ORF2 predicted a 24 kDa protein and the 435 bp long ORF3 predicted a 15 kDa protein. These predicted protein sequences exhibited 32-38% and 24-36% identity, respectively, with ExbB and ExbD proteins of three other bacteria. Thus, the sequence comparison identified the ORF1, ORF2 and ORF3 as gonococcal homologues of the *E. coli* tonB, exbB and exbD genes. An insertional mutation in the tonB homologue resulted in the failure of gonococci to grow with TF, LF or human haemoglobin (HB) as sole Fe sources and in the inability to take up ⁵⁵Fe from TF and LF. The tonB mutation did not prevent the utilization of Fe from citrate (CT) or haemin (HM). Binding of TF, LF and HB to whole cells in a solid-phase binding assay was largely unaffected by the tonB mutation. We conclude that the pathways for utilization of Fe bound to TF, LF and HB but not to HM or CT were dependent on the TonB system.

L7 ANSWER 19 OF 51 MEDLINE DUPLICATE 9
 ACCESSION NUMBER: 1998086208 MEDLINE
 DOCUMENT NUMBER: 98086208 PubMed ID: 9426239
 TITLE: The *Corynebacterium glutamicum* cglIM gene encoding a 5-cytosine methyltransferase enzyme confers a specific DNA methylation pattern in an McrBC-deficient *Escherichia coli* strain.
 AUTHOR: Schafer A; Tauch A; Droste N; Puhler A; Kalinowski J
 CORPORATE SOURCE: Department of Genetics, University of Bielefeld,

09/388090

SOURCE: Germany.
GENE, (1997 Dec 12) 203 (2) 95-101.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U13922
ENTRY MONTH: 199801
ENTRY DATE: Entered STN: 19980206
Last Updated on STN: 20000303
Entered Medline: 19980126

AB The cglIM gene of the coryneform soil bacterium *Corynebacterium glutamicum* ATCC 13032 has been cloned and characterized. The coding region comprises 1092 **nucleotides** and specifies a **protein** of 363 amino acid residues with a deduced Mr of 40700. The amino acid sequence showed striking similarities to methyltransferase enzymes generating 5-methylcytosine residues, especially to M x NgoVII from *Neisseria gonorrhoeae* recognizing the sequence GCSGC. The cglIM gene is organized in an unusual operon which contains, in addition, two genes **encoding** stress-sensitive restriction enzymes. Using PCR techniques the entire gene including the promoter region was amplified from the wild-type chromosome and cloned in *Escherichia coli*. Expression of the cglIM gene in *E. coli* under the control of its own promoter conferred the *C. glutamicum*-specific methylation pattern to co-resident shuttle plasmids and led to a 260-fold increase in the transformation rate of *C. glutamicum*. In addition, the methylation pattern produced by this methyltransferase enzyme is responsible for the sensitivity of **DNA** from *C. glutamicum* to the modified cytosine restriction (Mcr) system of *E. coli*.

L7 ANSWER 20 OF 51 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 1998072426 MEDLINE
DOCUMENT NUMBER: 98072426 PubMed ID: 9409768
TITLE: Evidence for two types of subunits in the bacterioferritin of *Magnetospirillum magnetotacticum*.
AUTHOR: Bertani L E; Huang J S; Weir B A; Kirschvink J L
CORPORATE SOURCE: Division of Biology, California Institute of Technology, Pasadena 91125, USA..
lebert@cco.caltech.edu
CONTRACT NUMBER: ES06652 (NIEHS)
SOURCE: GENE, (1997 Nov 12) 201 (1-2) 31-6.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF001959
ENTRY MONTH: 199801
ENTRY DATE: Entered STN: 19980130
Last Updated on STN: 19980130
Entered Medline: 19980121

AB In order to investigate the role of bacterioferritin (Bfr) in the biomineralization of magnetite by microorganisms, we have cloned and sequenced the bfr genes from *M. magnetotacticum*. The organism has two bfr genes that overlap by one **nucleotide**. Both **encode** putative **protein** products of 18 kDa, the

expected size for Bfr subunits, and show a strong similarity to other Bfr subunit **proteins**. By scanning the **DNA** sequence databases, we found that a limited number of other organisms, including *N. gonorrhoea*, *P. aeruginosa*, and *Synechocystis* PCC6803, also have two bfr genes. When the sequences of a number of microbial Bfrs are compared with each other, they fall into two distinct types with the organisms mentioned above having one of each type. Differences in heme- and metal-binding sites and ferroxidase activities of the two types of subunits are discussed.

L7 ANSWER 21 OF 51 MEDLINE DUPLICATE 11
 ACCESSION NUMBER: 96355882 MEDLINE
 DOCUMENT NUMBER: 96355882 PubMed ID: 8751920
 TITLE: Identification of an outer membrane protein involved in utilization of hemoglobin-haptoglobin complexes by nontypeable *Haemophilus influenzae*.
 AUTHOR: Maciver I; Latimer J L; Liem H H; Muller-Eberhard U; Hrkal Z; Hansen E J
 CORPORATE SOURCE: Department of Microbiology, University of Texas Southwestern Medical Center, Dallas 75235-9048, USA.
 CONTRACT NUMBER: AI17621 (NIAID)
 SOURCE: DK30203 (NIDDK)
 SOURCE: INFECTION AND IMMUNITY, (1996 Sep) 64 (9) 3703-12. Journal code: 0246127. ISSN: 0019-9567.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U43198
 ENTRY MONTH: 199610
 ENTRY DATE: Entered STN: 19961015
 Last Updated on STN: 19961015
 Entered Medline: 19961003

AB A recombinant plasmid containing a 6.5-kb fragment of nontypeable *Haemophilus influenzae* (NTHI) chromosomal **DNA** was shown to confer a hemoglobin-haptoglobin-binding phenotype on *Escherichia coli*. Use of a mini-Tn10kan transposon for random insertion mutagenesis of this recombinant plasmid allowed localization of the NTHI **DNA** responsible for this hemoglobin-haptoglobin-binding phenotype to a 3.5-kb PstI-XhoI fragment within the 6.5-kb NTHI **DNA** insert. When this mutagenized NTHI **DNA** fragment was used to transform the wild-type NTHI strain, the resultant kanamycin-resistant mutant exhibited significantly decreased abilities to bind hemoglobin-haptoglobin and utilize it as a source of heme for aerobic growth in vitro. This mutant also lacked expression of a 115-kDa outer membrane **protein** that was present in the wild-type parent strain. Transformation of this mutant with wild-type NTHI chromosomal **DNA** restored the abilities to bind and utilize hemoglobin-haptoglobin and to express the 115-kDa outer membrane **protein**. **Nucleotide** sequence analysis of the relevant NTHI **DNA** revealed the presence of a gene, designated *hhuA*, that **encoded** a predicted 117,145-Da **protein**. The *HhuA* **protein** exhibited features typical of a TonB-dependent outer membrane receptor and had significant identity with the hemoglobin receptors of both *Haemophilus ducreyi* and *Neisseria meningitidis*.

09/388090

L7 ANSWER 22 OF 51 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 96400835 MEDLINE
DOCUMENT NUMBER: 96400835 PubMed ID: 8807211
TITLE: Antigenic diversity of meningococcal outer membrane protein PorA has implications for epidemiological analysis and vaccine design.
AUTHOR: Feavers I M; Fox A J; Gray S; Jones D M; Maiden M C
CORPORATE SOURCE: Division of Bacteriology, National Institute for Biological Standards and Control, Potters Bar, Hertfordshire, United Kingdom.
SOURCE: CLINICAL AND DIAGNOSTIC LABORATORY IMMUNOLOGY, (1996 Jul) 3 (4) 444-50.
Journal code: 9421292. ISSN: 1071-412X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 19970219
Entered Medline: 19970131
AB The currently used serological subtyping scheme for the pathogen **Neisseria meningitidis** is not comprehensive, a proportion of isolates are reported as not subtypeable (NST), and few isolates are fully characterized with two subtypes for each strain. To establish the reasons for this and to assess the effectiveness of **DNA**-based subtyping schemes, dot blot hybridization and **nucleotide** sequence analyses were used to characterize the genes **encoding** antigenic variants of the meningococcal subtyping antigen, the PorA **protein**. A total of 233 strains, including 174 serologically NST and 59 partially or completely subtyped meningococcal strains, were surveyed. The NST isolates were chosen to be temporally and geographically representative of NST strains, isolated in England and Wales, and submitted to the Meningococcal Reference Unit in the period 1989 to 1991. The **DNA**-based analyses demonstrated that all of the strains examined possessed a porA gene. Some of these strains were serologically NST because of a lack of monoclonal antibodies against certain PorA epitopes; in other cases, strains expressed minor variants of known PorA epitopes that did not react with monoclonal antibodies in serological assays. Lack of expression remained a possible explanation for serological typing failure in some cases. These findings have important implications for epidemiological analysis and vaccine design and demonstrate the need for genetic characterization, rather than phenotypic characterization using monoclonal antibodies, for the identification of meningococcal strains.

L7 ANSWER 23 OF 51 MEDLINE DUPLICATE 13
ACCESSION NUMBER: 97149301 MEDLINE
DOCUMENT NUMBER: 97149301 PubMed ID: 8996109
TITLE: Molecular cloning and expression of NlaIII restriction-modification system in *E. coli*.
AUTHOR: Morgan R D; Camp R R; Wilson G G; Xu S Y
CORPORATE SOURCE: New England Biolabs Inc., Beverly, MA 01915, USA.
SOURCE: GENE, (1996 Dec 12) 183 (1-2) 215-8.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U59398
 ENTRY MONTH: 199702
 ENTRY DATE: Entered STN: 19970227
 Last Updated on STN: 19970227
 Entered Medline: 19970213

AB The NlaIII restriction enzyme isolated from *Neisseria lactamica* recognizes the sequence 5'-CATG-3', cleaving after the G to generate a four base 3' overhang. The NlaIII methylase and a portion of the NlaIII endonuclease gene were cloned into *E. coli* by the methylase selection method, and the remaining portion of the NlaIII endonuclease gene was cloned by inverse PCR. The **nucleotide** sequence of the endonuclease gene and the methylase gene were determined. The NlaIII endonuclease gene is 693 bp, **encoding** a **protein** with predicted molecular weight of 26487. The NlaIII methylase gene was identical with that previously reported [Labbe, D., Joltke, H.J. and Lau, P.C. (1990) Cloning and characterization of two tandemly arranged DNA methyltransferase genes of *Neisseria lactamica*: an adenine-specific M.NlaIII and a cytosine-type methylase. Mol. Gen. Genet. 224, 101-110]. The endonuclease and methylase genes overlap by four bases and are transcribed in the same orientation. The endonuclease gene was cloned into an improved T7 vector, and a high level of NlaIII endonuclease expression was achieved in *E. coli*.

L7 ANSWER 24 OF 51 JICST-EPlus COPYRIGHT 2002 JST
 ACCESSION NUMBER: 960623267 JICST-EPlus
 TITLE: Molecular Biological Analysis of the Component Proteins of the Adhesin Complex from Periodontopathogenic *Eikenella corrodens*.
 AUTHOR: YUMOTO HIROMICHI
 CORPORATE SOURCE: Univ. of Tokushima, Sch. of Dent.
 SOURCE: Shikoku Shigakkai Zasshi (Shikoku Dental Research), (1996) vol. 9, no. 1, pp. 19-42. Journal Code: L0495A (Fig. 19, Ref. 53)
 CODEN: SSZAED; ISSN: 0914-6091
 PUB. COUNTRY: Japan
 DOCUMENT TYPE: Journal; Article
 LANGUAGE: Japanese
 STATUS: New

AB *Eikenella corrodens* 1073 has a cell-associated N-acetyl-D-galactosamine-specific lectin-like substance (EcLS), which mediates the adherence of this bacteria to various host tissue cell surfaces. In this study, we cloned the genes **encoding** two component **proteins** of EcLS. EcLS migrated as **proteins** of about 300 and 45kDa upon SDS-PAGE under reducing conditions. At first, we cloned the gene **encoding** this 45kDa **protein** using a polymerase chain reaction and Southern hybridization. This gene was cloned into the expression vector pET22b (+) and the recombinant plasmid was transformed into *Escherichia coli* BL21 (DE3). Then, the expression of the cloned gene was induced with isopropyl- β -D-thiogalactopyranoside. The expressed 45kDa **protein** was purified after solubilization of inclusion bodies with urea and DEAE-Sepharose column chromatography. The **nucleotides** of this cloned fragments

were sequenced and an open reading frame (ORF) was found. This ORF comprised 990 **nucleotides** and encoded a **polypeptide** of 330 amino acids (Mr, 35, 748). The amino acid sequence deduced from the **nucleotide** sequence was highly homologous to those of the porins of **Neisserial** species. Subsequently, we cloned the gene **encoding** the **protein** reacting with the anti-EcLS monoclonal antibody from a gene bank, produced from *E. corrodens* 1073 chromosomal **DNA** in *E. coli* JM109. SDS-PAGE analysis revealed that clones produce three *Eikenella* **proteins** of about 60kDa, 25kDa and 10kDa, and immunoblot analysis revealed that the 25kDa **protein** reacts with the monoclonal antibody. The **nucleotides** of this cloned fragment were sequenced and an ORF was found. This ORF comprised 678 **nucleotides** and encoded a **polypeptide** of 226 amino acids (Mr, 24,586). The amino acid sequence deduced from the **nucleotide** sequence had no homology to any previously sequenced **proteins**. (author abst.)

L7 ANSWER 25 OF 51 MEDLINE DUPLICATE 14
 ACCESSION NUMBER: 96037800 MEDLINE
 DOCUMENT NUMBER: 96037800 PubMed ID: 7565116
 TITLE: Characterization of the pilF-pilD pilus-assembly locus of *Neisseria gonorrhoeae*.
 AUTHOR: Freitag N E; Seifert H S; Koomey M
 CORPORATE SOURCE: Department of Microbiology and Immunology, University of Michigan Medical School, Ann Arbor 48109-0620, USA.
 CONTRACT NUMBER: AI27837 (NIAID)
 AI31494 (NIAID)
 AI33493 (NIAID)
 +
 SOURCE: MOLECULAR MICROBIOLOGY, (1995 May) 16 (3) 575-86.
 Journal code: 8712028. ISSN: 0950-382X.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199511
 ENTRY DATE: Entered STN: 19951227
 Last Updated on STN: 19990129
 Entered Medline: 19951108

AB Expression of Type IV pili by the bacterial pathogen *Neisseria gonorrhoeae* appears to be essential for colonization of the human host. Several *N. gonorrhoeae* gene products have been recently identified which bear homology to **proteins** involved in pilus assembly and **protein** export in other bacterial systems. We report here the isolation and characterization of transposon insertion mutants in *N. gonorrhoeae* whose phenotypes indicate that the *N. gonorrhoeae* pilF and pilD gene products are required for gonococcal pilus biogenesis. Mutants lacking the pilD gene product, a pre-pilin peptidase, were unable to process the pre-pilin subunit into pilin and thus were non-piliated. pilF mutants processed pilin but did not assemble the mature subunit. Both classes of mutants released S-pilin, a soluble, truncated form of the pilin subunit previously correlated with defects in pilus assembly. In addition, mutants containing

transposon insertions in pilD or in a downstream gene, orfX, exhibited a severely restricted growth phenotype. Deletion analysis of pilD indicated that the poor growth phenotype observed for the pilD transposon mutants was a result of polar effects of the insertions on orfX expression. orfX **encodes** a predicted **polypeptide** of 23 kDa which contains a consensus **nucleotide**-binding domain and has apparent homologues in *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Thermus thermophilus*, and the eukaryote *Caenorhabditis elegans*. Although expression of orfX and pilD appears to be transcriptionally coupled, mutants containing transposon insertions in orfX expressed pili. Unlike either pilF or pilD mutants, orfX mutants were also competent for **DNA** transformation.

L7 ANSWER 26 OF 51 MEDLINE DUPLICATE 15
 ACCESSION NUMBER: 96117604 MEDLINE
 DOCUMENT NUMBER: 96117604 PubMed ID: 8559801
 TITLE: Genetic analysis of the minimal replicon of plasmid pIP417 and comparison with the other **encoding** 5-nitroimidazole resistance plasmids from *Bacteroides* spp.
 AUTHOR: Haggoud A; Trinh S; Moumni M; Reyssset G
 CORPORATE SOURCE: Unite des Anaerobies, Institut Pasteur, Paris, France.
 SOURCE: PLASMID, (1995 Sep) 34 (2) 132-43.
 Journal code: 7802221. ISSN: 0147-619X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-X86701; GENBANK-X86702; GENBANK-X87253
 ENTRY MONTH: 199602
 ENTRY DATE: Entered STN: 19960312
 Last Updated on STN: 19960312
 Entered Medline: 19960226

AB The **nucleotide** sequence of the **DNA** replication origin region of a *Bacteroides vulgatus* plasmid, pIP417, **encoding** 5-nitroimidazole resistance has been determined. This region of 1934 bp presents some characteristics similar to those of other replication **protein**-dependent origins. It contains a large open reading frame which could **encode** a basic Rep **protein** (RepA) of 36.8 kDa. Upstream of this ORF exist an AT-rich region, three direct repeats (iterons) of 21 bp, multiple DnaA binding sites, and sites, and sites for the integration host factor (IHF). Moreover, the amino acid sequence of the pIP417 RepA **protein** shows similarities with those of other Rep **proteins encoded** by plasmids of gram-negative bacteria: pR01600 from *Pseudomonas aeruginosa*; pPS10 from *Pseudomonas syringae*; pFA3 from *Neisseria gonorrhoeae*; and two cryptic plasmids from *Campylobacter hyointestinalis* and *Butyrivibrio fibrisolvens*. Although RepA can be expressed in an *Escherichia coli* in vitro transcription-translation assay, vectors containing the pIP417 replication origin did not replicate in *E. coli*. The homology of the pIP417 replication region with the corresponding regions of other *Bacteroides* spp. plasmids was also studied by Southern blot hybridization. The results indicated that the repA gene of plasmid pIP417 is homologous to that of plasmid pIP421, but not of plasmid pIP419. The replication region

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of plasmid pIP421 was sequenced and showed about 80% identity at the **nucleotide** level with that of pIP417. A small (3634-bp) cloning vector (pFK12) of entirely defined **nucleotide** sequence was constructed for *Bacteroides* spp.

L7 ANSWER 27 OF 51 MEDLINE DUPLICATE 16
ACCESSION NUMBER: 94321329 MEDLINE
DOCUMENT NUMBER: 94321329 PubMed ID: 8045888
TITLE: Molecular cloning and analysis of genes for sialic acid synthesis in *Neisseria meningitidis* group B and purification of the meningococcal CMP-NeuNAc synthetase enzyme.
AUTHOR: Ganguli S; Zapata G; Wallis T; Reid C; Boulnois G; Vann W F; Roberts I S
CORPORATE SOURCE: Department of Microbiology, University of Leicester, United Kingdom.
SOURCE: JOURNAL OF BACTERIOLOGY, (1994 Aug) 176 (15) 4583-9. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X78068
ENTRY MONTH: 199408
ENTRY DATE: Entered STN: 19940909
Last Updated on STN: 19980206
Entered Medline: 19940830

AB The gene **encoding** for the CMP-NeuNAc synthetase enzyme of *Neisseria meningitidis* group B was cloned by complementation of a mutant of *Escherichia coli* defective for this enzyme. The gene (*neuA*) was isolated on a 4.1-kb fragment of meningococcal chromosomal **DNA**. Determination of the **nucleotide** sequence of this fragment revealed the presence of three genes, termed *neuA*, *neuB*, and *neuC*, organized in a single operon. The presence of a truncated *ctrA* gene at one end of the cloned **DNA** and a truncated gene **encoding** for the meningococcal sialyltransferase at the other confirmed that the cloned **DNA** corresponded to region A and part of region C of the meningococcal capsule gene cluster. The predicted amino acid sequence of the meningococcal NeuA **protein** was 57% homologous to that of NeuA, the CMP-NeuNAc synthetase **encoded** by *E. coli* K1. The predicted molecular mass of meningococcal NeuA **protein** was 24.8 kDa, which was 6 kDa larger than that formerly predicted (U. Edwards and M. Frosch, FEMS Microbiol. Lett. 96:161-166, 1992). Purification of the recombinant meningococcal NeuA **protein** together with determination of the N-terminal amino acid sequence confirmed that this 24.8-kDa **protein** was indeed the meningococcal CMP-NeuNAc synthetase. The predicted amino acid sequences of the two other **encoded proteins** were homologous to those of the NeuC and NeuB **proteins** of *E. coli* K1, two **proteins** involved in the synthesis of NeuNAc. These results indicate that common steps exist in the biosynthesis of NeuNAc in these two microorganisms.

L7 ANSWER 28 OF 51 MEDLINE DUPLICATE 17
ACCESSION NUMBER: 95012644 MEDLINE
DOCUMENT NUMBER: 95012644 PubMed ID: 7927717
TITLE: Identification of a locus involved in the utilization

Searcher : Shears 308-4994

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of iron by *Haemophilus influenzae*.
AUTHOR: Sanders J D; Cope L D; Hansen E J
CORPORATE SOURCE: Department of Microbiology, University of Texas
Southwestern Medical Center, Dallas 75235-9048.
CONTRACT NUMBER: AI17621 (NIAID)
AI23366 (NIAID)
NCI CA09082-19 (NCI)
SOURCE: INFECTION AND IMMUNITY, (1994 Oct) 62 (10) 4515-25.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199411
ENTRY DATE: Entered STN: 19941222
Last Updated on STN: 19970203
Entered Medline: 19941104

AB *Haemophilus influenzae* has an absolute requirement for heme for aerobic growth. This organism can satisfy this requirement by synthesizing heme from iron and protoporphyrin IX (PPIX). *H. influenzae* type b (Hib) strain DL42 was found to be unable to form single colonies when grown on a medium containing free iron and PPIX in place of heme. In contrast, the nontypeable *H. influenzae* (NTHI) strain TN106 grew readily on the same medium. A genomic library from NTHI strain TN106 was used to transform Hib strain DL42, and recombinants were selected on a medium containing iron and PPIX in place of heme. A recombinant plasmid with an 11.5-kb NTHI DNA insert was shown to confer on Hib strain DL42 the ability to grow on iron and PPIX. Nucleotide sequence analysis revealed that this NTHI DNA insert contained three genes, designated *hitA*, *hitB*, and *hitC*, which encoded products similar to the *SfuABC* proteins of *Serratia marcescens*, which have been shown to constitute a periplasmic binding protein-dependent iron transport system in this enteric organism. The NTHI *HitA* protein also was 69% identical to the ferric-binding protein of *Neisseria gonorrhoeae*. Inactivation of the cloned NTHI *hitC* gene by insertion of an antibiotic resistance cartridge eliminated the ability of the recombinant plasmid to complement the growth deficiency of Hib DL42. Construction of an isogenic NTHI TN106 mutant lacking a functional *hitC* gene revealed that this mutation prevented this strain from growing on a medium containing iron and PPIX in place of heme. This NTHI *hitC* mutant was also unable to utilize either iron bound to transferrin or iron chelates. These results suggest that the products encoded by the *hitABC* genes are essential for the utilization of iron by NTHI.

L7 ANSWER 29 OF 51 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 94178945 MEDLINE
DOCUMENT NUMBER: 94178945 PubMed ID: 8132344
TITLE: Isolation and characterization of a gene involved in hemagglutination by an avian pathogenic *Escherichia coli* strain.
AUTHOR: Provence D L; Curtiss R 3rd
CORPORATE SOURCE: Department of Biology, Washington University, St. Louis, Missouri 63130.
CONTRACT NUMBER: AI28487 (NIAID)
SOURCE: INFECTION AND IMMUNITY, (1994 Apr) 62 (4) 1369-80.

Searcher : Shears 308-4994

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JOURNAL CODE: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
JOURNAL; ARTICLE; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L27423
ENTRY MONTH: 199404
ENTRY DATE: Entered STN: 19940428
Last Updated on STN: 19990129
Entered Medline: 19940421

AB In this article, we report the isolation and characterization of a gene that may be important in the adherence of avian pathogenic *Escherichia coli* to the avian respiratory tract. The *E. coli* strain HB101, which is unable to agglutinate chicken erythrocytes, was transduced with cosmid libraries from the avian pathogenic *E. coli* strain chi 7122. Enrichment of transductants that could agglutinate chicken erythrocytes yielded 19 colonies. These isolates contained cosmids that encompassed four nonoverlapping regions of the *E. coli* chromosome. Only one group of cosmids, represented by pYA3104, would cause *E. coli* CC118 to agglutinate chicken erythrocytes. A 10-kb fragment of this cosmid was subcloned in pACYC184. Transposon mutagenesis of this fragment with Tn5seq1 indicated that a contiguous 4.4-kb region of cloned **DNA** was required for hemagglutination. In vitro transcription/translation assays indicated that this 4.4-kb region of **DNA encoded** one **protein** of approximately 140 kDa. The **nucleotide** sequence of this region was determined and found to **encode** one open reading frame of 4,134 **nucleotides** that would **encode a protein** of 1,377 amino acids with a deduced molecular weight of 148,226. This gene confers on *E. coli* K-12 a temperature-sensitive hemagglutination phenotype that is best expressed when cells are grown at 26 degrees C, and we have designated this gene *tsh* and the deduced gene product Tsh. Insertional mutagenesis of the chromosomal *tsh* gene in chi 7122 had no effect on hemagglutination titers. The deduced **protein** was found to contain significant homology to the *Haemophilus influenzae* and *Neisseria gonorrhoeae* immunoglobulin A1 proteases. These data indicate that (i) a single gene isolated from the avian pathogenic *E. coli* strain chi 7122 will confer on *E. coli* K-12 a hemagglutination-positive phenotype, (ii) chi 7122 contains at least two distinct mechanisms to allow hemagglutination to occur, and (iii) the hemagglutinin Tsh has homology with a class of **proteins** previously not known to exist in *E. coli*.

L7 ANSWER 30 OF 51 MEDLINE DUPLICATE 19
ACCESSION NUMBER: 94156449 MEDLINE
DOCUMENT NUMBER: 94156449 PubMed ID: 8112835
TITLE: Identification and characterization of the *Treponema pallidum* tpn50 gene, an ompA homolog.
AUTHOR: Hardham J M; Stamm L V
CORPORATE SOURCE: Department of Microbiology and Immunology, School of Medicine, University of North Carolina, Chapel Hill 27599.
CONTRACT NUMBER: 1 U01 AI31496 (NIAID)
3 T32 AI07001 (NIAID)
AI24976 (NIAID)
SOURCE: INFECTION AND IMMUNITY, (1994 Mar) 62 (3) 1015-25.

Searcher : Shears 308-4994

PUB. COUNTRY: Journal code: 0246127. ISSN: 0019-9567.
 United States
 LANGUAGE: Journal; Article; (JOURNAL ARTICLE)
 English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U02628
 ENTRY MONTH: 199403
 ENTRY DATE: Entered STN: 19940406
 Last Updated on STN: 19940406
 Entered Medline: 19940330

AB *Treponema pallidum* is a pathogenic spirochete that has no known genetic exchange mechanisms. In order to identify treponemal genes **encoding** surface and secreted **proteins**, we carried out TnpH mutagenesis of a *T. pallidum* genomic **DNA** library in *Escherichia coli*. Several of the resulting clones expressed enzymatically active *T. pallidum*-alkaline phosphatase fusion **proteins**. The **DNA** sequence of the 5' portion of a number of the treponemal genes was obtained and analyzed. A recombinant clone harboring plasmid p4A2 that **encoded** a treponemal **protein** with an approximate molecular mass of 50,000 Da was identified. Plasmid p4A2 contained an open reading frame of 1,251 **nucleotides** that resulted in a predicted **protein** of 417 amino acids with a calculated molecular mass of 47,582 Da. We have named this gene tpn50 in accordance with the current nomenclature for *T. pallidum* genes. A 1.9-kb HincII-ClaI fragment from p4A2 that contained the tpn50 gene was subcloned to produce p4A2HC2. Comparison of the predicted amino acid sequence of Tpn50 with **protein** sequences in the National Center for Biotechnology Information data base indicated statistically significant homology to the *Pseudomonas* sp. OprF, *E. coli* OmpA, *Bordetella avium* OmpA, *Neisseria meningitidis* RmpM, *Neisseria gonorrhoeae* PIII, *Haemophilus influenzae* P6, *E. coli* PAL, and *Legionella pneumophila* PAL **proteins**. These **proteins** are all members of a family of outer membrane **proteins** that are present in gram-negative bacteria. The tpn50 gene complemented *E. coli* ompA mutations on the basis of two separate criteria. First, morphometry and electron microscopy data showed that *E. coli* C386 (ompA lpp) cells harboring plasmid vector pEBH21 were rounded while cells of the same strain harboring p4A2HC2 (Tpn50+), pWW2200 (OprF+), or pRD87 (OmpA+) were rod shaped. Second, *E. coli* BRE51 (MC4100 delta sulA-ompA) cells harboring pEBH21 grew poorly at 42 degrees C in minimal medium, while the growth of BRE51 cells harboring p4A2HC2 was similar to that of the parental MC4100 cells. These results demonstrate that the Tpn50 **protein** is functionally equivalent to the *E. coli* OmpA **protein**. If Tpn50 functions in a similar fashion in *T. pallidum*, then it may be localized to the treponemal outer membrane.

L7 ANSWER 31 OF 51 MEDLINE DUPLICATE 20
 ACCESSION NUMBER: 95198536 MEDLINE
 DOCUMENT NUMBER: 95198536 PubMed ID: 7891550
 TITLE: Lipooligosaccharide biosynthesis in *Neisseria gonorrhoeae*: cloning, identification and characterization of the alpha 1,5 heptosyltransferase I gene (rfaC).
 COMMENT: Erratum in: Mol Microbiol 1995 Apr;16(1):169
 AUTHOR: Zhou D; Lee N G; Apicella M A

09/388090

CORPORATE SOURCE: Department of Microbiology, University of Iowa, Iowa City 52242.
CONTRACT NUMBER: AI18384 (NIAID)
AI24616 (NIAID)
SOURCE: MOLECULAR MICROBIOLOGY, (1994 Nov) 14 (4) 609-18.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U10385
ENTRY MONTH: 199504
ENTRY DATE: Entered STN: 19950427
Last Updated on STN: 19960129
Entered Medline: 19950417

AB The identical partial deep-core structure of Hep alpha 1-3Hep alpha 1-5KDO in Salmonella typhimurium LT2 LPS and **Neisseria gonorrhoeae** LOS enabled us to isolate a DNA fragment from **N. gonorrhoeae** that was able to complement the alpha 1,5 LOS heptosyltransferase defect in the S. typhimurium rfaC630 (SA1377) mutant. SDS-PAGE analysis confirmed the production of wild-type LPS in the transformant. Subcloning revealed that complementation was due to a 1.2 kb fragment. Sequence analysis revealed a complete open reading frame capable of **encoding** a 36-37 kDa **peptide**. In vitro transcription-translation analysis of the 1.2 kb clone confirmed that a 37 kDa **protein** was **encoded** by this DNA fragment. The DNA sequence-deduced **protein** had 36% identity and 58% similarity to S. typhimurium heptosyltransferase I (RfaC). Primer extension analysis indicated that transcription of the cloned gene in **N. gonorrhoeae** strain 1291 begins 144 bp upstream of the start codon at a G **nucleotide**. An isogenic mutant of **N. gonorrhoeae** strain 1291 with an m-Tn3 insertion inside the coding sequence expressed a single truncated LOS with a similar molecular mass to S. typhimurium rfaC LPS. We conclude that the 1.2 kb fragment **encodes** the alpha 1,5 LOS heptosyltransferase I (RfaC) in **N. gonorrhoeae**. Our studies also provide further evidence that the third KDO residue in S. typhimurium LPS is added after the core synthesis is completed.

L7 ANSWER 32 OF 51 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 94336757 MEDLINE
DOCUMENT NUMBER: 94336757 PubMed ID: 8058819
TITLE: Deletion and transposon mutagenesis and sequence analysis of the pR01600 OriR region found in the broad-host-range plasmids of the pQF series.
AUTHOR: Jansons I; Touchie G; Sharp R; Almquist K; Farinha M A; Lam J S; Kropinski A M
CORPORATE SOURCE: Department of Microbiology and Immunology, Queen's University, Kingston, Ontario, Canada.
SOURCE: PLASMID, (1994 May) 31 (3) 265-74.
Journal code: 7802221. ISSN: 0147-619X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L22691

Searcher : Shears 308-4994

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ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19940920
Last Updated on STN: 19940920
Entered Medline: 19940914

AB The **nucleotide** sequence of the replicative origin (OriR) region of the small cryptic broad-host-range plasmid, pRO1600, which forms the basis of a number of useful cloning vectors has been determined. In addition it has been subjected to Tn5 mutagenesis, deletion analysis, and subcloning in order to define the regions essential for replication in *Pseudomonas aeruginosa*. The sequence (1894 bp) contains a fragment derived from transposon Tn1. The OriR region is structurally related to other replication (Rep) **protein**-dependent origins in that it has an A-T-rich region upstream of four 17-bp direct repeats (iterons) which presumably function in initiator **protein** binding. The sequence also contains a **DNA**-A-binding site and an open reading frame which could **encode** a basic (pI 10.6) 25,343-Da Rep **protein** with homology to RepA from the *Neisseria gonorrhoeae* beta-lactamase plasmid pFA3. The possible evolutionary origin of this plasmid in *P. aeruginosa* (RP1) is discussed.

L7 ANSWER 33 OF 51 MEDLINE DUPLICATE 22
ACCESSION NUMBER: 95075307 MEDLINE
DOCUMENT NUMBER: 95075307 PubMed ID: 7984102
TITLE: Variable expression of the Opc outer membrane protein in *Neisseria meningitidis* is caused by size variation of a promoter containing poly-cytidine.
AUTHOR: Sarkari J; Pandit N; Moxon E R; Achtman M
CORPORATE SOURCE: Max-Planck Institut fur molekulare Genetik, Berlin, Germany.
SOURCE: MOLECULAR MICROBIOLOGY, (1994 Jul) 13 (2) 207-17.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199501
ENTRY DATE: Entered STN: 19950116
Last Updated on STN: 19950116
Entered Medline: 19950105

AB Opa **proteins** of *Neisseria meningitidis* exhibit translational phase variation via addition or deletion of repetitive coding repeat units within the **DNA encoding** the **protein** leader sequence. In contrast, Opc phase variation is the result of transcriptional regulation. Transcription starts 13 **nucleotides** after the -10 region of an unusual promoter sequence containing a variable number of contiguous cytidine residues and lacking a -35 region. Efficient expression of Opc occurred in strains with 12 to 13 cytidine residues, intermediate expression in strains with 11 or 14 residues and no expression with < or = 10 or > or = 15 residues. This unusual regulation may have evolved because the Opc **protein** enables meningococcal invasion and is immunogenic.

L7 ANSWER 34 OF 51 MEDLINE DUPLICATE 23
ACCESSION NUMBER: 95131727 MEDLINE
DOCUMENT NUMBER: 95131727 PubMed ID: 7830552

Searcher : Shears 308-4994

09/388090

TITLE: Molecular analysis of the biosynthesis pathway of the
alpha-2,8 polysialic acid capsule by *Neisseria*
meningitidis serogroup B.
AUTHOR: Edwards U; Muller A; Hammerschmidt S; Gerardy-Schahn
R; Frosch M
CORPORATE SOURCE: Institute fur Medizinische Mikrobiologie,
Medizinische Hochschule Hannover, Germany.
SOURCE: MOLECULAR MICROBIOLOGY, (1994 Oct) 14 (1) 141-9.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199502
ENTRY DATE: Entered STN: 19950307
Last Updated on STN: 19950307
Entered Medline: 19950222

AB The genes **encoding** all enzymes necessary for capsular
polysaccharide biosynthesis in *Neisseria meningitidis* B
are located on a 5 kb DNA fragment within the chromosomal
cps gene cluster. **Nucleotide** sequence analysis revealed
four open reading frames (ORFs), which can **encode**
proteins with molecular masses of 41.4 kDa, 24.9 kDa, 38.3
kDa, and 54.4 kDa, respectively. These ORFs constitute a
transcriptional unit as demonstrated by Northern blots. Primer
extension analysis revealed that the transcriptional start site is
preceded by a **nucleotide** sequence with homologies to the
sigma 70 consensus promoter sequence of *Escherichia coli*. Functional
analysis of the **proteins encoded** by the ORFs
indicated that ORF2 **encodes** the CMP-NeuNAc synthetase,
ORF3 **encodes** the NeuNAc condensing enzyme, and ORF4
encodes the alpha-2,8 polysialyltransferase. ORF1
encodes an enzyme, which provides a precursor molecule for
synthesis of monomeric NeuNAc. In *E. coli* the subcloned ORFs 2-4
were able to synthesize a high-molecular-weight alpha-2,8 polysialic
acid. In contrast, inactivation of ORF1 in the meningococcal genome
resulted in a complete loss of capsule production. A regulatory
enzyme, the CMP-NeuNAc hydrolase, which cleaves CMP-NeuNAc to CMP
and NeuNAc, was not found as a part of the capsular polysaccharide
biosynthesis gene operon or within the cps gene cluster.

L7 ANSWER 35 OF 51 MEDLINE DUPLICATE 24
ACCESSION NUMBER: 95075288 MEDLINE
DOCUMENT NUMBER: 95075288 PubMed ID: 7984085
TITLE: Cloning and sequencing of *Vibrio cholerae*
mannose-sensitive haemagglutinin pilin gene:
localization of mshA within a cluster of type 4 pilin
genes.
AUTHOR: Jonson G; Lebens M; Holmgren J
CORPORATE SOURCE: Department of Medical Microbiology and Immunology,
Goteborg University, Sweden.
SOURCE: MOLECULAR MICROBIOLOGY, (1994 Jul) 13 (1) 109-18.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X77217

Searcher : Shears 308-4994

09/388090

ENTRY MONTH: 199412
ENTRY DATE: Entered STN: 19950116
Last Updated on STN: 19961015
Entered Medline: 19941230

AB The mannose-sensitive haemagglutinin (MSHA) pilus that is associated with *Vibrio cholerae* strains of El Tor biotype has been shown to be a potential colonization factor and protective antigen. The gene **encoding** the structural subunit of MSHA pili was cloned from size-fractionated *SacI*-cleaved chromosomal **DNA** in the expression phage vector lambda ZAPII. Positive clones carried a c. 5.3 kb *SacI* fragment and were identified on the basis of MSHA expression and hybridization with a synthetic oligonucleotide probe based upon the N-terminus of MshA, the structural subunit of MSHA. The mshA gene was localized to a 2.6 kb *SalI*-*EcoRI* fragment, which was subcloned and shown to express MshA from its own promoter in *Escherichia coli*. **Nucleotide** sequencing of the entire fragment revealed six open reading frames (ORFs) of which four were complete. The mshA gene **encodes** an 18,094 Da prepilin **protein**, which in its mature form has a size of 17,436 Da. MshA is a type 4 (N-MePhe) pilin **protein** that is more homologous to pilins produced by *Pseudomonas aeruginosa* and *Neisseria gonorrhoeae* than to TcpA, the structural subunit of the toxin-coregulated pilus of *V. cholerae*. The **protein** seems to be directly involved in receptor binding, as an in-frame mutation in the mshA gene was found to abolish both D-mannose-dependent haemagglutination and binding of *V. cholerae* bacteria to D-mannose-containing agarose beads. Three additional ORFs, all in the same transcriptional orientation as mshA, were found to **encode** type 4 pilin-like **proteins**. A potential promoter with a sequence homologous to that of cAMP-CRP-activated promoters in *E. coli* was identified upstream of ORF3, the gene preceding mshA.

L7 ANSWER 36 OF 51 MEDLINE DUPLICATE 25
ACCESSION NUMBER: 95058178 MEDLINE
DOCUMENT NUMBER: 95058178 PubMed ID: 7526119
TITLE: Expression of meningococcal epitopes in LamB of *Escherichia coli* and the stimulation of serosubtype-specific antibody responses.
AUTHOR: McCarvil J; McKenna A J; Grief C; Hoy C S; Sesardic D; Maiden M C; Feavers I M
CORPORATE SOURCE: Division of Bacteriology, National Institute for Biological Standards and Control, South Mimms, Hertfordshire, UK.
SOURCE: MOLECULAR MICROBIOLOGY, (1993 Oct) 10 (1) 203-13.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199411
ENTRY DATE: Entered STN: 19950110
Last Updated on STN: 19960129
Entered Medline: 19941129

AB The class 1 outer membrane **protein** (OMP), a major variable surface antigen of *Neisseria meningitidis*, is a component of novel meningococcal vaccines currently in field trials. Serological variants of the **protein** are also used to

serosubtype meningococci. Most of the amino acid changes that give rise to antigenic variants of the **protein** occur in two variable regions (VR1 and VR2) that are thought to form loops on the cell surface. The polymerase chain reaction (PCR) was used to amplify the **nucleotide** sequences **encoding** VR1 and VR2 from the chromosomal **DNA** of *N. meningitidis* strain M1080. These were cloned in frame into the *lamB* gene of the *Escherichia coli* expression vector pAJC264. Whole-cell enzyme-linked immunosorbent assays (ELISAs), using monoclonal antibodies, and SDS-PAGE confirmed that, upon induction, strains of *E. coli* carrying these constructs expressed hybrid *LamB* **proteins** containing the *N. meningitidis* surface loops. These strains were used to immunize rabbits and the resultant polyclonal antisera reacted specifically with the class 1 OMP of reference strain M1080 (P1.7). Immunogold labelling of meningococcal cells and whole-cell dot-blot analyses with these antisera showed that the variable epitopes were exposed on the cell surface and confirmed that this approach could be used to obtain serosubtype-specific antisera. The binding profiles of the antisera were determined from their reactions with overlapping synthetic **peptides** and their reactivity compared with that of relevant serosubtype-specific monoclonal antibodies. This approach was used successfully to raise antisera against two other class 1 OMP VR2s. A fourth antiserum raised against a VR2, including the P1.1 epitope, was not subtype specific.

L7 ANSWER 37 OF 51 MEDLINE DUPLICATE 26
 ACCESSION NUMBER: 93345825 MEDLINE
 DOCUMENT NUMBER: 93345825 PubMed ID: 8344530
 TITLE: Cloning and characterization of *Neisseria meningitidis* genes **encoding** the transferrin-binding proteins Tbp1 and Tbp2.
 AUTHOR: Legrain M; Mazarin V; Irwin S W; Bouchon B; Quentin-Millet M J; Jacobs E; Schryvers A B
 CORPORATE SOURCE: Transgene, Strasbourg, France.
 SOURCE: GENE, (1993 Aug 16) 130 (1) 73-80.
 PUB. COUNTRY: Netherlands
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-L03653; GENBANK-L03654; GENBANK-L07632; GENBANK-M96932; GENBANK-M96933; GENBANK-S65693; GENBANK-S65694; GENBANK-X54209; GENBANK-Z15129; GENBANK-Z15130; GENBANK-Z35133
 ENTRY MONTH: 199309
 ENTRY DATE: Entered STN: 19930924
 Last Updated on STN: 19950206
 Entered Medline: 19930903

AB Genes *tbp1* and *tbp2*, **encoding** the transferrin-binding **proteins** Tbp1 and Tbp2, have been isolated from two strains of *Neisseria meningitidis*. The *tbp2* and *tbp1* open reading frames are tandemly arranged in the genome with an 87-bp intergenic region, and the **DNA** region upstream from the *tbp2*-coding sequence contains domains homologous to *Escherichia coli* promoter consensus motives. **Nucleotide** sequence analysis suggests the existence of a Tbp1 precursor carrying an N-terminal signal **peptide** with a peptidase I cleavage site and of a Tbp2 precursor with N-terminal homology to lipoproteins, including a

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peptidase II cleavage site. Comparison of the Tbp1 deduced amino acid (aa) sequences from both strains showed about 76% aa homology, while those of Tbp2 revealed only about 47% aa homology. These comparisons should be extended to other *Neisseria* strains in order to evaluate further this genetic divergence further.

L7 ANSWER 38 OF 51 MEDLINE DUPLICATE 27
ACCESSION NUMBER: 94010340 MEDLINE
DOCUMENT NUMBER: 94010340 PubMed ID: 8406039
TITLE: Natural variation of the NgoII restriction-modification system of *Neisseria gonorrhoeae*.
AUTHOR: Gunn J S; Stein D C
CORPORATE SOURCE: Department of Microbiology, University of Maryland, College Park 20742.
CONTRACT NUMBER: AI 24452 (NIAID)
SOURCE: GENE, (1993 Sep 30) 132 (1) 15-20.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L12963; GENBANK-L14564; GENBANK-L24523; GENBANK-L24524; GENBANK-L24525; GENBANK-L24526; GENBANK-L24527; GENBANK-L24528; GENBANK-L24529; GENBANK-X65556
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19980206
Entered Medline: 19931119

AB The NgoII restriction-modification (R-M) system of *Neisseria gonorrhoeae* recognizes the sequence 5'-GGCC-3'. This system is **encoded** by two separate genes, dcmB for the methyltransferase (MTase) and dcrB for the restriction endonuclease (ENase). Three strains that vary in their NgoII phenotype were examined. Strain Pgh3-2 produced detectable levels of both enzymes, strain F62 lacked detectable levels of the dcrB gene product, and strain WR302 failed to produce either gene product. Strains that lacked either enzyme activity still possessed the genes that **encode** them. Transcriptional fusions of dcrB in strains F62 and Pgh3-2 indicate that this gene is transcribed at nearly identical levels in each strain. The **DNA encoding** the NgoII R-M system was cloned from the three strains, and the **nucleotide** sequence was determined. The dcrB genes of WR302 and F62 possess the same frameshift mutation (base position 1435) which would result in a truncated **protein**. The WR302 dcmB was found to have a point mutation that changed Arg288 (a residue that is conserved in all prokaryotic and phage cytosine MTases sequenced to date) to Trp.

L7 ANSWER 39 OF 51 MEDLINE DUPLICATE 28
ACCESSION NUMBER: 95058171 MEDLINE
DOCUMENT NUMBER: 95058171 PubMed ID: 7968509
TITLE: Analysis in *Neisseria meningitidis* and other *Neisseria* species of genes homologous to the FKBP immunophilin family.
AUTHOR: McAllister C F; Stephens D S
CORPORATE SOURCE: Department of Medicine, Emory University School of Medicine, Atlanta, Georgia.

Searcher : Shears 308-4994

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SOURCE: MOLECULAR MICROBIOLOGY, (1993 Oct) 10 (1) 13-23.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199411
ENTRY DATE: Entered STN: 19950110
Last Updated on STN: 19970203
Entered Medline: 19941129

AB The immunophilin family of FK506-binding **proteins** (FKBPs), involved in eukaryotic **protein**-folding and cell regulation, have recently been found to have prokaryotic homologues. Genes with sequences homologous to those **encoding** human FKBP were examined in *Neisseria* species. An FKBP **DNA** sequence was present, as shown by the polymerase chain reaction and Southern blotting experiments, in the chromosome of *Neisseria meningitidis* (14 strains) and in all 11 different commensal *Neisseria* spp. studied, but was not found in *Neisseria gonorrhoeae* (11 strains tested) or in *Moraxella catarrhalis*. The **nucleotide** and predicted **protein** sequences of the FKBP-**encoding** domain from five of the meningococcal strains were highly conserved (e.g. > or = 97% homologous). The meningococcal **nucleotide** sequence was > or = 93% homologous and the consensus meningococcal **protein** sequence was > or = 97% homologous to FKBP sequences found in seven different commensal *Neisseria* spp. The meningococcal **nucleotide** and predicted **protein** sequences were > or = 59% homologous to the conserved C-terminus of the human FKBP gene family. The FKBP **nucleotide** sequence was present as a single copy in the chromosome of commensal *Neisseria* spp. and in most strains of *N. meningitidis*. The FKBP gene was linked to the silent pilin locus, pilS, in class II-piliated meningococcal strains. In meningococcal strains expressing class I pili, the FKBP gene was linked to one of several pilS loci but not the pilE locus present in these strains. FKBP genes found in commensal *Neisseria* spp. were not linked to known pilin loci.

L7 ANSWER 40 OF 51 MEDLINE DUPLICATE 29
ACCESSION NUMBER: 93194072 MEDLINE
DOCUMENT NUMBER: 93194072 PubMed ID: 8449408
TITLE: Characterization of the replication region of the small cryptic plasmid of *Campylobacter hyointestinalis*.
AUTHOR: Waterman S R; Hackett J; Manning P A
CORPORATE SOURCE: Department of Microbiology and Immunology, University of Adelaide, Australia.
SOURCE: GENE, (1993 Mar 15) 125 (1) 11-7.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L03653; GENBANK-L03654; GENBANK-M91441;
GENBANK-X54203; GENBANK-X54204; GENBANK-X54205;
GENBANK-X54206; GENBANK-X54207; GENBANK-X54208;
GENBANK-X54209

Searcher : Shears 308-4994

09/388090

ENTRY MONTH: 199304
ENTRY DATE: Entered STN: 19930423
Last Updated on STN: 19950206
Entered Medline: 19930413

AB The complete **nucleotide** sequence of a 2.5-kb cryptic plasmid from *Campylobacter hyointestinalis* was determined. Only one open reading frame (ORF), **encoding a polypeptide** of M(r) 39,667, designated RepA, could be identified within the sequence. This was confirmed by minicell analysis. Analysis of the region upstream from the ORF showed an A+T-rich region followed by four 19-bp direct repeats. Together, these features are characteristic of other replication origins (ori(s)). The promoter sequence of the repA gene was identified by primer extension analysis and both the putative -10 and -35 regions were found to lie within two potential hairpin-loop structures. RepA showed marked amino acid sequence homology to a replication-initiation **protein** from the *Neisseria gonorrhoeae* plasmid, pFA3, and with other replication-initiation **proteins** over two conserved motifs. A putative partitioning (par) locus was identified upstream from the ori and consisted of a perfect 9-bp inverted repeat and six putative **DNA** gyrase-binding sites. A putative mobilization origin (oriT) region was identified. This featured a 19-bp imperfect inverted repeat adjacent to a sequence of 12 bp which showed strong homology to the consensus sequence of the 'nick regions' in a variety of oriTs of other plasmids.

L7 ANSWER 41 OF 51 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 1992-299974 [36] WPIDS
CROSS REFERENCE: 1999-008809 [01]
DOC. NO. NON-CPI: N1992-229717
DOC. NO. CPI: C1992-133797
TITLE: Polypeptide(s) **encoded** by PILC1 or PILC2
of NEISSERIA GONORRHOEAE - for diagnosis of and
vaccination against NEISSERIA infections.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): JONSSON, A; NORMARK, S
PATENT ASSIGNEE(S): (UNIW) UNIV WASHINGTON
COUNTRY COUNT: 35
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9213871	A1	19920820	(199236)*	EN	122
RW: AT BE CH DE DK ES FR GB GR IT LU MC NL OA SE					
W: AT AU BB BG BR CA CH CS DE DK ES FI GB HU JP KP KR LK LU MG					
MN MW NL NO PL RO RU SD SE					
AU 9214114	A	19920907	(199249)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9213871	A1	WO 1992-US863	19920131
AU 9214114	A	AU 1992-14114	19920131
		WO 1992-US863	19920131

FILING DETAILS:

Searcher : Shears 308-4994

09/388090

PATENT NO	KIND	PATENT NO
AU 9214114	A Based on	WO 9213871

PRIORITY APPLN. INFO: US 1991-648781 19910131

AN 1992-299974 [36] WPIDS

CR 1999-008809 [01]

AB WO 9213871 A UPAB: 19990107

The following are claimed: (A) a recombinant polynucleotide **encoding a polypeptide** comprising an immunoreactive epitope of a **protein encoded in pilC of Neisseria**; (B) a vector comprising a recombinant polynucleotide as in (A); (C) a host cell transformed with a vector as in (B); (D) a recombinant expression system comprising a polynucleotide as in (A) operably linked to a control sequence compatible with a desired host; (E) a cell transformed with a recombinant expression system as in (D); (F) a **polypeptide** produced by a cell as in (E); (G) a purified **polypeptide** comprising an immunoreactive epitope of a **protein encoded in pilC of Neisseria**; (H) a recombinant **polypeptide** comprising an immunoreactive epitope of a **protein encoded in pilC of Neisseria**; (I) a compsn. comprising purified polyclonal anti-PilC antibodies, where the pilC is of **Neisseria**; (J) a compsn. comprising a monoclonal antibody (MAb) directed against an immunoreactive epitope **encoded in pilC of Neisseria**; (K) an oligomer capable of hybridising to a sequence in pilC of **Neisseria**, where the oligomer comprises a pilC sequence complementary to at least 6 contiguous **nucleotides** of pilC; (L) a recombinant polynucleotide comprising a **DNA** sequence of at least 8 contiguous **nucleotides** from pilC where the pilC sequence is as shown.

USE - The polynucleotides, polypeptides and antibodies can be used, opt. in the form of kits, in the detection of pilC or anti-pilC antibodies for the diagnosis of pathogenic microorganisms contg. type 4 pil
Dwg.0/7

L7	ANSWER 42 OF 51	MEDLINE	DUPLICATE 30
ACCESSION NUMBER:	93077456	MEDLINE	
DOCUMENT NUMBER:	93077456	PubMed ID: 1447140	
TITLE:	Cloning and sequencing of a gene encoding a 21-kilodalton outer membrane protein from Bordetella avium and expression of the gene in Salmonella typhimurium.		
AUTHOR:	Gentry-Weeks C R; Hultsch A L; Kelly S M; Keith J M; Curtiss R 3rd		
CORPORATE SOURCE:	Laboratory of Microbial Ecology, National Institute of Dental Research, Bethesda, Maryland 20892.		
CONTRACT NUMBER:	1-F32-AI-07628 (NIAID) AI-28487 (NIAID)		
SOURCE:	JOURNAL OF BACTERIOLOGY, (1992 Dec) 174 (23) 7729-42. Journal code: 2985120R. ISSN: 0021-9193.		
PUB. COUNTRY:	United States Journal; Article; (JOURNAL ARTICLE)		
LANGUAGE:	English		
FILE SEGMENT:	Priority Journals		

Searcher : Shears 308-4994

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OTHER SOURCE: GENBANK-L01135; GENBANK-L01136; GENBANK-L01137;
GENBANK-L01138; GENBANK-L01139; GENBANK-L01140;
GENBANK-L01141; GENBANK-M96550; GENBANK-M98391;;
GENBANK-Z11768

ENTRY MONTH: 199212

ENTRY DATE: Entered STN: 19930129
Last Updated on STN: 19970203
Entered Medline: 19921230

AB Three gene libraries of *Bordetella avium* 197 DNA were prepared in *Escherichia coli* LE392 by using the cosmid vectors pCP13 and pYA2329, a derivative of pCP13 specifying spectinomycin resistance. The cosmid libraries were screened with convalescent-phase anti-*B. avium* turkey sera and polyclonal rabbit antisera against *B. avium* 197 outer membrane proteins. One *E. coli* recombinant clone produced a 56-kDa protein which reacted with convalescent-phase serum from a turkey infected with *B. avium* 197. In addition, five *E. coli* recombinant clones were identified which produced *B. avium* outer membrane proteins with molecular masses of 21, 38, 40, 43, and 48 kDa. At least one of these *E. coli* clones, which encoded the 21-kDa protein, reacted with both convalescent-phase turkey sera and antibody against *B. avium* 197 outer membrane proteins. The gene for the 21-kDa outer membrane protein was localized by Tn5seq1 mutagenesis, and the nucleotide sequence was determined by dideoxy sequencing. DNA sequence analysis of the 21-kDa protein revealed an open reading frame of 582 bases that resulted in a predicted protein of 194 amino acids. Comparison of the predicted amino acid sequence of the gene encoding the 21-kDa outer membrane protein with protein sequences in the National Biomedical Research Foundation protein sequence data base indicated significant homology to the OmpA proteins of *Shigella dysenteriae*, *Enterobacter aerogenes*, *E. coli*, and *Salmonella typhimurium* and to *Neisseria gonorrhoeae* outer membrane protein III, *Haemophilus influenzae* protein P6, and *Pseudomonas aeruginosa* porin protein F. The gene (ompA) encoding the *B. avium* 21-kDa protein hybridized with 4.1-kb DNA fragments from EcoRI-digested, chromosomal DNA of *Bordetella pertussis* and *Bordetella bronchiseptica* and with 6.0- and 3.2-kb DNA fragments from EcoRI-digested, chromosomal DNA of *B. avium* and *B. avium*-like DNA, respectively. A 6.75-kb DNA fragment encoding the *B. avium* 21-kDa protein was subcloned into the Asd+ vector pYA292, and the construct was introduced into the avirulent delta cya delta crp delta asd *S. typhimurium* chi 3987 for oral immunization of birds. The gene encoding the 21-kDa protein was expressed equivalently in *B. avium* 197, delta asd *E. coli* chi 6097, and *S. typhimurium* chi 3987 and was localized primarily in the cytoplasmic membrane and outer membrane. (ABSTRACT TRUNCATED AT 400 WORDS)

L7 ANSWER 43 OF 51 MEDLINE DUPLICATE 31
ACCESSION NUMBER: 92363557 MEDLINE
DOCUMENT NUMBER: 92363557 PubMed ID: 1500170
TITLE: Molecular analysis of the serotyping antigens of
Neisseria meningitidis.
AUTHOR: Feavers I M; Suker J; McKenna A J; Heath A B; Maiden

Searcher : Shears 308-4994

09/388090

CORPORATE SOURCE: M C
Division of Bacteriology and Informatics Laboratory,
National Institute for Biological Standards and
Control, South Mimms, Potters Bar, Hertfordshire,
United Kingdom.
SOURCE: INFECTION AND IMMUNITY, (1992 Sep) 60 (9) 3620-9.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199209
ENTRY DATE: Entered STN: 19920925
Last Updated on STN: 19920925
Entered Medline: 19920917

AB Molecular approaches to the rapid analysis of the serotyping
antigens of *Neisseria meningitidis*, the class 2 and 3
outer membrane **proteins** (OMPs), were developed, evaluated,
and used to study 12 antigenic variants of these **proteins**.
A primer set for the polymerase chain reaction (PCR) amplification
of the genes **encoding** these antigens was devised.
Low-stringency amplification of meningococcal chromosomal
DNA with this primer set resulted in the amplification of
two products from each strain, whereas at higher stringencies only
one product was amplified in most strains. Southern hybridization
techniques and restriction analyses were used to differentiate the
PCR products amplified at high stringencies from strains expressing
class 2 or class 3 OMPs; these PCR products were further
characterized by the determination of their **nucleotide**
sequences, confirming that they represented the amplified class 2
and class 3 OMP genes. Analyses of these and other
nucleotide sequences enabled the construction of a phenogram
illustrating the interrelationships between *Neisseria* OMP
genes. The comparative analysis of deduced amino acid sequences
revealed conserved and variable regions of the **proteins**;
the latter probably correspond to surface loops on the
protein and hence are potentially exposed to the immune
system. Further analyses of the primary structures of these related
porins from *Neisseria* species enabled construction of
models of the secondary structure of these antigens and comparison
of these models with those previously published. The methods
reported in the present work are rapid reproducible procedures for
the analysis of antigenic variants of these **proteins**.

L7 ANSWER 44 OF 51 MEDLINE DUPLICATE 32
ACCESSION NUMBER: 93084746 MEDLINE
DOCUMENT NUMBER: 93084746 PubMed ID: 1452652
TITLE: Identification of meningococcal serosubtypes by
polymerase chain reaction.
AUTHOR: Maiden M C; Bygraves J A; McCarvil J; Feavers I M
CORPORATE SOURCE: National Institute for Biological Standards and
Control, Potters Bar, Hertfordshire, United Kingdom.
SOURCE: JOURNAL OF CLINICAL MICROBIOLOGY, (1992 Nov) 30 (11)
2835-41.
Journal code: 7505564. ISSN: 0095-1137.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

Searcher : Shears 308-4994

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FILE SEGMENT: Priority Journals
ENTRY MONTH: 199301
ENTRY DATE: Entered STN: 19930129
Last Updated on STN: 19930129
Entered Medline: 19930106

AB The polymerase chain reaction was used as the basis of a novel typing method for *Neisseria meningitidis*. Southern hybridization experiments demonstrated that it was possible to identify genes **encoding** different serological variants of the meningococcal class 1 outer membrane **protein** by probing with polymerase chain reaction products corresponding to known epitopes. A set of 14 defined variable regions was prepared in bacteriophage M13mp19 by the cloning of polymerase chain reaction products. The phage were dot blotted onto membrane filters, which were used as targets for hybridization of radiolabeled amplified class 1 outer membrane **protein** genes. Thus, the presence of many different subtype-specific epitopes could be investigated in one experiment. This technique was evaluated with a set of serological reference strains, mainly of serogroup B organisms, and provided an alternative, rapid, and comprehensive typing system that was capable of distinguishing known serosubtypes and also of defining currently untypeable strains independently of sodium dodecyl sulfate-polyacrylamide gel electrophoresis or serological analysis. An additional advantage of this technique was that in the case of an unknown serosubtype (i.e., one that did not hybridize with any of the known samples), the **DNA** amplified from the original sample could be used to determine the **nucleotide** sequence of the novel serosubtype and to clone the corresponding variable region into bacteriophage M13. It may be possible to develop this procedure for the diagnostic detection and typing of meningococci directly from clinical samples even when culture is not possible because of antibiotic treatment of an acute case.

L7 ANSWER 45 OF 51 MEDLINE DUPLICATE 33
ACCESSION NUMBER: 92210515 MEDLINE
DOCUMENT NUMBER: 92210515 PubMed ID: 1339419
TITLE: Sequence analysis and complementation studies of the argJ gene **encoding** ornithine acetyltransferase from *Neisseria gonorrhoeae*.
AUTHOR: Martin P R; Mulks M H
CORPORATE SOURCE: Department of Microbiology and Public Health, Michigan State University, East Lansing 48824-1101.
CONTRACT NUMBER: A1-21264
SOURCE: JOURNAL OF BACTERIOLOGY, (1992 Apr) 174 (8) 2694-701.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M65216; GENBANK-M79364; GENBANK-M79365;
GENBANK-M79366; GENBANK-M79367; GENBANK-M79368;
GENBANK-M79369; GENBANK-M79370; GENBANK-M79371;
GENBANK-M79372
ENTRY MONTH: 199205
ENTRY DATE: Entered STN: 19920515
Last Updated on STN: 19920515
Entered Medline: 19920506

AB Clinical isolates of *Neisseria gonorrhoeae*

Searcher : Shears 308-4994

frequently are deficient in arginine biosynthesis. These auxotrophs often have defects in the fifth step of the arginine biosynthetic pathway, the conversion of acetylornithine to ornithine. This reaction is catalyzed by the enzyme ornithine acetyltransferase, which is a product of the *argJ* gene. We have cloned and sequenced the gonococcal *argJ* gene and found that it contains an open reading frame of 1,218 **nucleotides** and **encodes** a **peptide** with a deduced Mr of 42,879. This predicted size was supported by minicell analysis. This gene was capable of complementing both *Escherichia coli* *argE* and *argA* mutations and of transforming an *ArgJ*⁻ strain of *N. gonorrhoeae* to *Arg*⁺. Southern blots were able to detect bands that specifically hybridized to the gonococcal *argJ* gene in genomic **DNA** from *Pseudomonas aeruginosa* but not *E. coli*, a result that reflects the divergent nature of the arginine biosynthetic pathway in these organisms.

L7 ANSWER 46 OF 51 MEDLINE DUPLICATE 34
 ACCESSION NUMBER: 92219993 MEDLINE
 DOCUMENT NUMBER: 92219993 PubMed ID: 1560777
 TITLE: Role of horizontal genetic exchange in the antigenic variation of the class 1 outer membrane protein of *Neisseria meningitidis*.
 AUTHOR: Feavers I M; Heath A B; Bygraves J A; Maiden M C
 CORPORATE SOURCE: Division of Bacteriology, National Institute for Biological Standards and Control, Potters Bar, Hertfordshire, UK.
 SOURCE: MOLECULAR MICROBIOLOGY, (1992 Feb) 6 (4) 489-95. Journal code: 8712028. ISSN: 0950-382X.
 PUB. COUNTRY: ENGLAND: United Kingdom
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199205
 ENTRY DATE: Entered STN: 19920529
 Last Updated on STN: 19920529
 Entered Medline: 19920514
 AB The **nucleotide** sequences of the genes **encoding** the class 1 outer membrane **protein** of *Neisseria meningitidis* (PorA) from 15 meningococcal isolates have been examined. These strains, isolated over a number of years, represented a variety of serological types, clonal groups, and geographical locations. Analysis of the aligned **nucleotide** sequences showed that the known serological relationships between these **proteins** were not necessarily reflected throughout the **nucleotide** sequences of their genes. The uneven distribution of base substitutions, revealed by a comparison of the informative bases, suggested that these genes possessed a mosaic structure. This structure probably resulted from the horizontal transfer of **DNA** between strains and would have contributed to both the generation and the spread of novel antigenic variants of the **protein**. In addition, the **nucleotide** differences between *porA* genes from different strains were not consistent with the **nucleotide** sequence divergence of the whole chromosome, as indicated by pulsed-field gel electrophoresis (PFGE) fingerprinting techniques: some strains with divergent PFGE fingerprints shared *porA* genes with extensive regions of **nucleotide** sequence identity and, conversely, some strains

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with similar chromosome structures possessed porA genes with different **nucleotide** sequences and serological properties. This suggested that entire genes had been exchanged between strains. Given that the meningococcal class 1 OMP is a major component in novel vaccines, some of which are currently undergoing field trials, the potential of horizontal genetic exchange to generate antigenic diversity has implications for the design of such vaccines.

L7 ANSWER 47 OF 51 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 1991-255062 [35] WPIDS
DOC. NO. CPI: C1991-110615
TITLE: DNA from Neisseria meningitidis - used to prepare probes for detecting Neisseriaceae and for producing recombinant protein.
DERWENT CLASS: B04 D16
INVENTOR(S): MCFADDEN, J
PATENT ASSIGNEE(S): (UYSU-N) UNIV SURREY
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
GB 2241242	A	19910828	(199135)*		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
GB 2241242	A	GB 1990-572	19900110

PRIORITY APPLN. INFO: GB 1990-572 19900110

AN 1991-255062 [35] WPIDS

AB GB 2241242 A UPAB: 19930928

The following are claimed: (A) plasmid pUS210; (B) a **nucleotide** sequence which has greater than 70% homology to a sequence of 30bp contained in the repetitive element which is present in **Neisseria meningitidis** strain 43 and is contained partly or wholly in plasmid pUS210; (C) a **nucleotide** sequence which has greater than 70% homology to a sequence of 30bp contained in the **neisseria DNA** of plasmid pUS210; (D) a bacterium, virus or eukaryotic cell which contains as a result of genetic modification a **nucleotide** sequence as in (B) or (C); (E) **protein encoded** by a **nucleotide** sequence as in (B) or (C) and produced by a genetically modified organism as in (D).

USE - Nucleotide sequence can be used to prepare probes to differentiate specifically strains of Neisseriaceae and for the detection, identification and genetic typing of Neisseria meningitidis and Neisseria gonorrhoea. Recombinant protein obtd. using the nucleotide sequence can be used to provide diagnostic or immunological reagents.

In an example, a neisseria DNA library was constructed from Neisseria meningitidis strain 43 partially digested with Sau3A and cloned into the BamHI site of dephosphorylated pBR322. Ligation mixt. was transformed into E.coli strain PLK-F providing a methylcytosine-restriction background suitable for cloning neisseria DNA. Randomly isolated clones were tested for their ability to

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differentiate strains of *Neisseria meningitidis* in hybridisation experiments. Clones contg. repetitive DNA were isolated by screening the library using colony hybridisation with radio-labelled *mNeisseria meningitidis* DNA. Screening for repetitive DNA identified a clone of 2Kb present in plasmid pUS210 which hybridised with multiple fragments of *Neisseria meningitidis* strain G3 used in constructing the DNA library. *E. coli* contg. pUS210 was deposited as NCIMB 40247. @ (14pp Dwg.No.0/3)

L7 ANSWER 48 OF 51 MEDLINE DUPLICATE 35
ACCESSION NUMBER: 91260456 MEDLINE
DOCUMENT NUMBER: 91260456 PubMed ID: 1904526
TITLE: Comparison of the class 1 outer membrane proteins of eight serological reference strains of *Neisseria meningitidis*.
AUTHOR: Maiden M C; Suker J; McKenna A J; Bygraves J A; Feavers I M
CORPORATE SOURCE: National Institute for Biological Standards and Control, Hertfordshire, UK.
SOURCE: MOLECULAR MICROBIOLOGY, (1991 Mar) 5 (3) 727-36. Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X52371; GENBANK-X52372; GENBANK-X57177; GENBANK-X57178; GENBANK-X57179; GENBANK-X57180; GENBANK-X57181; GENBANK-X57182; GENBANK-X57183; GENBANK-X57184
ENTRY MONTH: 199107
ENTRY DATE: Entered STN: 19910802
Last Updated on STN: 19910802
Entered Medline: 19910717

AB Primers suitable for the amplification of the gene **encoding** the class 1 outer membrane **protein** of *Neisseria meningitidis* by the polymerase chain reaction (PCR) were designed from published **DNA** sequences and used to study the gene in eight meningococcal strains of different serogroup, serotype and subtype. At high annealing stringency one product, shown to correspond to the class 1 **protein** gene, was amplified from each strain. For three strains an additional smaller product, provisionally identified as the gene **encoding** the class 3 outer membrane **protein**, was amplified at lower annealing stringencies. **Nucleotide** sequence analysis of the PCR products corresponding to the class 1 **proteins** established the differences in the primary structure of the **proteins** between each of the subtypes and other outer-membrane **proteins** from *Neisseria* spp. These differences impose constraints on possible structural models of these **proteins**. Most amino acid sequence variation occurred in two domains of between 8 and 17 amino acids; there was an additional region which varied mainly between classes of outer membrane **protein** and there were nine conserved regions. Using appropriate primers it was possible to distinguish between class 1 outer membrane **protein** genes from strains of different subtypes by the PCR.

L7 ANSWER 49 OF 51 MEDLINE DUPLICATE 36

Searcher : Shears 308-4994

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ACCESSION NUMBER: 91033057 MEDLINE
DOCUMENT NUMBER: 91033057 PubMed ID: 2121620
TITLE: Sequence of the argF gene **encoding**
ornithine transcarbamoylase from *Neisseria*
gonorrhoeae.
AUTHOR: Martin P R; Cooperider J W; Mulks M H
CORPORATE SOURCE: Department of Microbiology and Public Health,
Michigan State University, East Lansing 48824.
CONTRACT NUMBER: AI-21264 (NIAID)
SOURCE: GENE, (1990 Sep 28) 94 (1) 139-40.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M34930
ENTRY MONTH: 199012
ENTRY DATE: Entered STN: 19910208
Last Updated on STN: 19910208
Entered Medline: 19901226

AB The gonococcal argF gene **encoding** ornithine
transcarbamoylase (OTCase) contains an open reading frame of 993
nucleotides which starts with a GUG codon and
encodes a peptide with a deduced Mr of 36,731. We
compared the predicted amino acid (aa) sequence to OTCase sequences
previously determined for *Escherichia coli* and *Pseudomonas*
aeruginosa and found that highly conserved regions in the genes from
these organisms were also conserved in *Neisseria*
gonorrhoeae, including those aa known to be important for
carbamoyl phosphate and ornithine binding. In the flanking regions
of the gene were found 15-bp inverted repeats that may serve as
transcriptional termination signals, and which contain the
neisserial DNA-uptake sequence.

L7 ANSWER 50 OF 51 MEDLINE DUPLICATE 37
ACCESSION NUMBER: 91117164 MEDLINE
DOCUMENT NUMBER: 91117164 PubMed ID: 2277628
TITLE: Cloning and characterization of two tandemly arranged
DNA methyltransferase genes of *Neisseria lactamica*:
an adenine-specific M.NlaIII and a cytosine-type
methylase.
AUTHOR: Labbe D; Holtke H J; Lau P C
CORPORATE SOURCE: Biotechnology Research Institute, National Research
Council of Canada, Montreal, Quebec.
SOURCE: MOLECULAR AND GENERAL GENETICS, (1990 Oct) 224 (1)
101-10.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199103
ENTRY DATE: Entered STN: 19910329
Last Updated on STN: 19980206
Entered Medline: 19910304

AB The gene **encoding** the *Neisseria*
lactamica III DNA methyltransferase (M.NlaIII)
which recognizes the sequence CATG has been cloned and expressed in

Escherichia coli. **DNA** sequencing of a 3.125 kb EcoRI-PstI fragment localizes the M. NlaIII gene to a 334 codon open reading frame (ORF) and identifies, 468 bp downstream, a second ORF of 313 amino acids, which is referred to as M.NlaX. Both **proteins** are detectable in the E. coli coupled in vitro transcription-translation system; they are apparently expressed from separate **N. lactamica** promoters. The N-terminal half of the previously characterized M.FokI, which methylates adenine in one of the **DNA** strands with its asymmetric recognition sequence (GGATG), is found to have 41% sequence identity and a further 11.7% sequence similarity with M.NlaIII. Among the conserved amino acids is the wellknown DPPY sequence motif. With one exception, analysis of the **nucleotides** coding for the DP dipeptide in all known DPPY sequences shows the presence of an inherent **DNA** adenine methylation (dam) recognition site of GATC. A low level of expression of M.NlaX in E. coli prevents the elucidation of its sequence recognition specificity. Sequence analysis of M.NlaX shows that it is closely related to the group of monospecific 5-methylcytosine **DNA** methyltransferases (M.EcoRII, Dcm, M.HpaII and M.HhaI) which all have a modified cytosine at the second position of the recognition sequences. Both M.EcoRII and Dcm amino acid sequences are about 50% identical with M.NlaX; a considerable degree of sequence identity is found in the so-called variable region which is believed to be responsible for sequence recognition specificity. M.NlaX is probably the counterpart to the E. coli Dcm in **N. lactamica**.

L7 ANSWER 51 OF 51 MEDLINE DUPLICATE 38
 ACCESSION NUMBER: 89173305 MEDLINE
 DOCUMENT NUMBER: 89173305 PubMed ID: 2538396
 TITLE: Primary structure of the porin protein of Haemophilus influenzae type b determined by nucleotide sequence analysis.
 AUTHOR: Hansen E J; Hasemann C; Clausell A; Capra J D; Orth K; Moomaw C R; Slaughter C A; Latimer J L; Miller E E
 CORPORATE SOURCE: Department of Microbiology, University of Texas Southwestern Medical Center, Dallas 75235.
 CONTRACT NUMBER: AI-17621 (NIAID)
 SOURCE: INFECTION AND IMMUNITY, (1989 Apr) 57 (4) 1100-7.
 Journal code: 0246127. ISSN: 0019-9567.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 198905
 ENTRY DATE: Entered STN: 19900306
 Last Updated on STN: 19970203
 Entered Medline: 19890505
 AB Sequencing techniques for single- and double-stranded **DNA** were used to determine the **nucleotide** sequence of the gene **encoding** P2, the major outer membrane (porin) **protein** of Haemophilus influenzae type b (Hib). The open reading frame **encoding** the P2 **protein** comprised 361 amino acid codons. Comparison of the inferred amino acid sequence with data obtained by amino acid sequencing of the N terminus of the mature or fully processed P2 **protein** revealed that this **protein** has a signal **peptide** composed of 20 amino acids. N-terminal amino acid sequencing of

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tryptic **peptides** derived from purified P2 allowed direct identification of 158 of the 341 amino acids in the fully processed P2 **protein**; there was 100% correlation between these amino acid sequences and that inferred from the **nucleotide** sequence. The amino acid sequence of Hib P2 **protein** had 23 to 25% homology with the sequence of the OmpF porin of Escherichia coli and with that of the **Neisseria gonorrhoeae** porin P.IA. Codon usage in the Hib P2 gene was significantly different from that observed for a gene **encoding** a porin of E. coli. **DNA** hybridization studies indicated that there is a single copy of the P2 gene in the Hib chromosome. The availability of the **nucleotide** and amino acid sequences for the Hib P2 **protein** will facilitate investigation of the antigenic characteristics and structure-function relationship of this porin.

FILE 'REGISTRY' ENTERED AT 12:32:40 ON 14 JUN 2002

L8 E SERINE PROTEASE/CN 5
175 S SERINE PROTEASE ?/CN
E SERINE PROTEINASE/CN 5
L9 131 S SERINE PROTEINASE ?/CN
L10 295 S L8 OR L9

FILE 'HCAPLUS' ENTERED AT 12:33:39 ON 14 JUN 2002

L8 175 SEA FILE=REGISTRY ABB=ON PLU=ON SERINE PROTEASE ?/CN
L9 131 SEA FILE=REGISTRY ABB=ON PLU=ON SERINE PROTEINASE ?/CN

L10 295 SEA FILE=REGISTRY ABB=ON PLU=ON L8 OR L9
L11 198 SEA FILE=HCAPLUS ABB=ON PLU=ON (L10 OR (SERINE OR
SER) (W) (PROTEINASE OR PROTEASE)) (S)MOTIF
L12 129602 SEA FILE=HCAPLUS ABB=ON PLU=ON ((NUCLEIC OR DNA OR
DEOXYRIBONUCLEIC OR DEOXY RIBONUCLEIC) AND NUCLEOTIDE)
AND (POLYPEPTIDE OR POLYPROTEIN OR PROTEIN OR PEPTIDE)
L13 49 SEA FILE=HCAPLUS ABB=ON PLU=ON L11 AND L12
L14 0 SEA FILE=HCAPLUS ABB=ON PLU=ON L13 AND (NEISSER? OR
(NEISSER? OR N) (W) (GONOCOCC? OR GONORRH? OR CATARRHAL?
OR LACTAMIC? OR OVIS OR LACUNATA OR BOVIS OR OSLOENSIS))

FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, JICST-EPLUS, JAPIO, CABA,

VETU, VETB, PHIC, PHIN, TOXCENTER' ENTERED AT 12:36:48 ON
14 JUN 2002)

L15 0 S L14

FILE 'HOME' ENTERED AT 12:38:05 ON 14 JUN 2002